

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 08:34:37 ; Search time 67 Seconds

(without alignments)
984.464 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTPLPYQTP.....KLNLFNIADAFVGDGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2593	100.0	495	23	Arabidopsis CDPK2
2	2458	94.8	501	21	Arabidopsis thalia
3	2458	94.8	501	23	Arabidopsis CDPK4
4	2064	79.6	425	21	Arabidopsis thalia
5	1932	74.5	512	20	Soybean CDPK prote
6	1924	74.2	399	21	Arabidopsis thalia
7	1742	67.2	483	21	Arabidopsis thalia
8	1742	67.2	556	21	Arabidopsis thalia
9	1703	65.7	856	21	Arabidopsis thalia
10	1703	65.7	893	21	Arabidopsis thalia

11	1703	65.7	1017	21	AA338597	Arabidopsis thalia
12	1509.5	58.2	549	23	AA52842	Physcomitrella pat
13	1509	58.2	408	21	AA331159	Arabidopsis thalia
14	1501	57.9	463	21	AA46565	Arabidopsis thalia
15	1500	57.8	280	22	AA665758	ATCDPK2 kinase dom
16	1462	56.4	529	21	AA229590	Arabidopsis thalia
17	1462	56.4	542	21	AA229589	Arabidopsis thalia
18	1460.5	56.3	459	21	AA229591	Arabidopsis thalia
19	1457	56.2	569	15	AA56237	protein kinase spe
20	1325.5	51.1	538	21	AA43621	Arabidopsis thalia
21	1319	50.9	404	21	AA46566	Arabidopsis thalia
22	1231	47.5	378	21	AA46567	Arabidopsis thalia
23	1187.5	45.8	307	20	AAW93255	Tobacco CDPK prote
24	1166.5	45.0	424	21	AA43622	Arabidopsis thalia
25	1153.5	44.5	421	21	AA43623	Arabidopsis thalia
26	1059	40.8	413	22	AA665755	ATCDPK kinase doma
27	1015.5	39.2	523	21	AA43621	Arabidopsis thalia
28	928.5	35.8	426	21	AA43622	Arabidopsis thalia
29	920.5	35.5	302	21	AA54428	zea mays protein f
30	900	34.7	274	22	AA665756	ATCDPK1 kinase dom
31	897	34.2	274	19	AAW49837	Amino acid sequenc
32	887	34.2	274	22	AA665757	ATCDPK1 kinase do
33	887	34.2	274	22	AA665759	ATCDPK1A PK domain
34	849	32.7	597	23	AA52841	Physcomitrella pat
35	842.5	32.5	384	21	AA43622	Arabidopsis thalia
36	829	32.0	623	22	AA85583	Rice CDPK (clone r
37	771.5	29.8	456	16	AA74996	E. maxima Em70-1 a
38	753.5	29.1	504	21	AA43623	Arabidopsis thalia
39	753.5	29.1	594	21	AA43622	Arabidopsis thalia
40	737	28.4	502	21	AA53884	Arabidopsis thalia
41	737	28.4	594	21	AA53883	Arabidopsis thalia
42	712.5	27.5	428	21	AA43622	Arabidopsis thalia
43	712.5	27.5	524	21	AA43622	Arabidopsis thalia
44	694.5	26.8	189	23	AA59978	Human DITP poly
45	690.5	26.6	414	21	AA53885	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAW48000
ID AAW48000 standard; Protein: 495 AA.

AC AAW48000;

XX 08-MAR-2002 (first entry)

DT Arabidopsis CDPK2 SEQ ID NO 1.

DE Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
KW disease resistance; agricultural; pathogen; crop yield; ornamental;
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
KW transgenic; plant; enzyme.

OS Arabidopsis thaliana.

XX WO200184911-A1.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US14368.

XX 05-MAY-2000; 2000US-201925P.

XX (GEO) GEN HOSPITAL CORP.

PI Sheen J;

DR WPI; 2002-062179/08.

XX N-PSDB; ABA06021.

PT Producing plant having increased disease resistance, comprises

PT regenerating plant from a non-naturally occurring plant cell
PT over-expressing a polynucleotide encoding a calcium dependent protein
PT kinase polypeptide
XX
PS Disclosure: Fig 1; 44pp; English.
XX
CC The invention relates to producing a plant having increased disease
CC resistance, comprising providing a non-naturally occurring plant cell
CC over-expressing a polynucleotide encoding a calcium dependent protein
CC kinase (CDPK) polypeptide and regenerating a plant from the plant
CC cell, where the CDPK polypeptide is expressed in the plant, increasing
CC the resistance of the plant to disease as compared to a
CC naturally-occurring plant. The method is useful for a variety of
CC agricultural and commercial purposes including improving a plant's
CC resistance against plant pathogens, increasing crop yields, improving
CC crop and ornamental quality and reducing agricultural production costs.
CC The method facilitates an effective and economical method for in-plant
CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g. application of fungicides,
CC bactericides, nematocides, insecticides, or viricides) that are typically
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis
CC thaliana CDPK2 of the invention.

XX Sequence 495 AA;

Query Match 100.0%; Score 2593; DB 23; Length 495;
Best Local Similarity 100.0%; Pred. No. 2e-222;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKENRPSNTVLPYOTPRLRDHYLLGKLGQGGFGTYLCTEKSTSANVACKSIPKR 60
DB 1 METKENRPSNTVLPYOTPRLRDHYLLGKLGQGGFGTYLCTEKSTSANVACKSIPKR 60
QY 61 KLVCRDIEDVWREIQIMHLSHPNVVRKGTYESDVHVMVEYCEGSELFDRIVSKG 120
DB 61 KLVCRDIEDVWREIQIMHLSHPNVVRKGTYESDVHVMVEYCEGSELFDRIVSKG 120
QY 121 HFSERAVKLIKITLGVWVACHSLGYMHRLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSERAVKLIKITLGVWVACHSLGYMHRLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180
QY 181 GOYLDVVGSPYVAPEVLKCYGPPIIDVWSAGVILYLLSGVPPFWAFTESGIFRQILQ 240
DB 181 GOYLDVVGSPYVAPEVLKCYGPPIIDVWSAGVILYLLSGVPPFWAFTESGIFRQILQ 240
QY 241 GKLDKSDPWPITSEAAKDLIYKMLRSPKRIISAHEALCHPWIVDEQAAPKPLDPAVL 300
DB 241 GKLDKSDPWPITSEAAKDLIYKMLRSPKRIISAHEALCHPWIVDEQAAPKPLDPAVL 300
QY 301 SRLKQFSQNMKIKKMLRVIAERLSEETGGELKEFKMIDTNSGTTITFEELKAGLKRVG 360
DB 301 SRLKQFSQNMKIKKMLRVIAERLSEETGGELKEFKMIDTNSGTTITFEELKAGLKRVG 360
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYIT 420
DB 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYIT 420
QY 421 IDELQSACTEFGLCDPLDDMIKEIDLNDGKIDFSEFTAMMKRGDVGSRRTMMKNLNF 480
DB 421 IDELQSACTEFGLCDPLDDMIKEIDLNDGKIDFSEFTAMMKRGDVGSRRTMMKNLNF 480
QY 481 NIADAFGVGDEKSD 495
DB 481 NIADAFGVGDEKSD 495

RESULT 2
AAG35776
ID AAG35776 standard; Protein: 501 AA.
XX
AC AAG35776;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 43753.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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Query Match 94.8%; Score 2458; DB 21; Length 501;		
Best Local Similarity 94.8%; Pred. No. 2.2e-210;		
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;		
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QY	64	CREDYEDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEVCEGELFDRIYSKGHFS 123
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Db	63	CREDYEDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEVCEGELFDRIYSKGHFS 122
QY	124	EREAKLIKTLGVVEACHSIGVMHRLKPNFLFSDPKDDAKLKATDFGLSVFKPGQY 183
		: : : : : : : : :
Db	123	EREAKLIKTLGVVEACHSIGVMHRLKPNFLFSDPKDDAKLKATDFGLSVFKPGQY 182

OS Arabidopsis thaliana.
XX
XX
PN EF1033405-A2.
XX
XX
PD 06-SEP-2000.
XX
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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DB	22	VLQRTQNIREVVEVGRKLGOGGFTTCTIRASGGCKFACKSPKRLKCKEDYEDVWR	81		
QY	74	EIQIMHLSHPNNVRIGKTYEDSVFHHIYMEVCEGGELEFDRIVSKGHFSEREAVKLIKT	133		
DB	82	EIQIMHLSHPNNVRIGKTYEDSVFHHIYMEVCEGGELEFDRIVSKGHFSEREAVKLIKT	141		
QY	134	ILGVVEACHSLGVMHRLDKPENLFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVGSPPY	193		
DB	142	IVEVVEACHSLGVMHRLDKPENLFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVGSPPY	201		
QY	194	VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETPESGTFROILOGKLDKSDPWTPI	253		
DB	202	VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETPESGTFROILOGKLDKSDPWTPI	261		
QY	254	SEAKDLIYKMLSPKRRISAHEALCHPWIVDEQAAPKPLDPVAVLSRLKQFSQMNKIK	313		
DB	262	SDSAKDLIRKMLDQNPTRLTATHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSQMNKIK	321		
QY	314	KMALRVTAERLSEEEIGGLKELFKMIDTNSGTITFEE---LKAGLKRVSSELMSEIK	369		
DB	322	KMALRVTAERLSEEEIGGLKELFKMIDTNSGTITFEE---LKAGLKRVSSELMSEIK	381		
QY	370	SLMDAADIDNSGTIDYGEFLAATLHMKNMEREEILVAASFDFDKDGGYITIDELQSACT	429		
DB	382	DLMDAADIDNSGTIDYGEFLAATLHMKNMEREEILVAASFDFDKDGGYITIDELQSACT	441		
QY	430	EFGLCDPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRMTMMKNLNFNTADAFV	488		
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XX	KW	Protein identification; signal transduction pathway; metabolic pathway;			
XX	KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
XX	KW	termination sequence.			
XX	OS	Arabidopsis thaliana.			
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.2%; Score 1742; DB 21; Length 483;
Best Local Similarity 68.4%; Pred. No. 1.5e-146;
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;

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DB 244 ESDPWPVSDSADKLIRRLMSKPAERLTAEHLRHPWCICNGVAPDRALDPAVLSRLKQ 303

QY 306 FSDNNKIKKNAVLIAERLSEIEIGLKFMDIDTNSGTITFEELKAGLKVGSSELM 365
DB 304 FSAMNKKKNAVLIAERLSEIEIGLKFMDIDTNSGTITFEELKAGLKVGSSELM 363

QY 366 SEIKSLMDAADIDNSTIDYGEFLAATLHNNKREIEILVAAFSDFDKGSGVITIDELQ 425
DB 364 TEIHLMDAADVNSTIDYSEFIATLHNNKREIEILVAAFSDFDKGSGVITIDELQ 423

QY 426 SACTEGLCDIPLDMMIKELDLNDGKIDFSEFTAMMRKGD-CVGRSRTMMKNLNFNIAD 484
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Qy 485 A 485
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Db 483 A 483

RESULT 8

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DT 17-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX

OS Arabidopsis thaliana.

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PN EP1033405-A2.

PD

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Query Match 67.2%; Score 1742; DB 21; Length 556;

Best Local Similarity 68.4%; Pred. No. 1.9e-146;

Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;

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Query Match 65.7%; Score 1703; DB 21; Length 1017;

Best Local Similarity 65.7%; Pred. No. 1.3e-142;

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DQ 629 GELFRIIQRGHYTERKAAELARTIVGLEACHSLGVHRLDKPENLDFVSEDSLLKT 688
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RESULT 12
AAM52842

ID AAM52842 standard; Protein; 549 AA.

AC AAM52842;

22-FEB-2002 (first entry)

Physcomitrella patens CPK-2 protein, SEQ ID NO:39.

Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
calcium-dependent protein kinase-2; CPK-2; overexpression;
environmental stress; salinity; drought; temperature; tolerance;
transgenic plant; EST; expressed sequence tag.

Physcomitrella patens.

WO2001177356-A2.

18-OCT-2001.

06-APR-2001; 2001WO-US11435.

07-APR-2000; 2000US-196001P.

(BADI) BASF PLANT SCI GMBH.

Da Costa Silva EO, Bohnert HJ, Van Thiel N, Chen R;

Sarría-Millán R;

WPI; 2002-049153/06.

N-PSDB; ABA91081.

New protein, useful for increasing tolerance to environmental stress,

comprises a Protein Kinase Stress-Related Protein selected from

Protein kinases, Casein kinase homologs, MAP kinases or Calcium
dependent protein kinases -
Claim 13: Fig 3M; 154pp; English.

Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
proteins (PKSRPs) from the moss *Physcomitrella patens*, and sequences
ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
sequences were obtained from expressed sequence tags (ESTs; ABA91056-
ABA91068) derived from *Physcomitrella patens* cDNA libraries. The PKSRPs
of the invention comprise protein kinase-6 (PK-6), protein kinase-7
(PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2),
MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),
calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein
kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer
tolerance to environmental stresses such as salinity, drought,
temperature, metal, chemical, pathogenic and oxidative stress.
Physcomitrella patens PKSRP nucleic acids may be used to generate
transgenic plants and seeds with increased tolerance to salinity, drought
and temperature. The transgenic plants generated can be monocots or
dicots and are especially maize, wheat, rye, oat, triticale, rice,
barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants
(e.g., soybean, peanut, vicia species, alfalfa), solanaceous plants
(e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea,
salix species, oil palm, coconut, perennial grasses and forage crops. The
PKSRP nucleotide and proteins may also be used in evolutionary and
protein structural studies and as markers for specific regions of
the genome.

Sequence 549 AA;

Query Match 58.2%; Score 1509.5; DB 23; Length 549;
Best Local Similarity 60.8%; Pred. No. 9.9e-126;
Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;

QY 5 PNPSPSNT--VLPYQTPRLDRHLLGKLGQGGTTLCTEKSTSNYACKSPKPK 61
DQ 69 PRPKPASVSGVLGKPLSDIRQSYILGELRGQFGVTYLCDTKMTNAYACKSAKRK 128
QY 62 LVCREDYEDVWRRIQIMHLSHPNVVRITKGTEDSVFVHIVMEVCEGGEFDRIVSKGH 121
DQ 129 LYSKEDIEDVKREVQIMHLSGTPNIVLKDVPEDKSHVHLMELCAGGELFDRIIAKH 188
QY 122 FSEREAVKLITILGVVEACHSLGVHRLDKPENLDFSPKDDAKLKATDFGLSVFKPG 181
DQ 189 YSERAADMCRIYVNVVHRCVHSLGVHRLDKPENLDFGLSKAETAPLKATDFGLSPKPG 248
QY 182 QYLYDVVGGSPYVAPEVLKKCYGPEIDVWSAGVILXILLSGVPPWAEETESGIRFOILQ 241
DQ 249 DVFDIVGSAYVAPEVLRKRYGPESDVWSAGVIVYILLSGVPPWAEETESGIRFOILQ 308
QY 242 KLDFKSDPWTISEAKDLIYKMLERSPKKRIASHEALCHPWIVDEQAAPKLPDPAVLS 301
DQ 309 HIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQVNLHPWMEKEDGADPVDNAVIL 368
QY 302 RLKQFSQMNKIKMALRVIAERLSEEEIGLKELFKMTIDTNSGTTITFEELKAGLKRYS 361
DQ 369 RLKQFSQMNKIKMALRVIAERLSEEEIGLKELFKMTIDTNSGTTITFEELKAGLKRYS 428
QY 362 ELMESEIKSLMDAADIDNSGTIDYGEFFLAATLHMNKEREELVAASDFDQSGYIT 421
DQ 429 KLNESDIRKLEAADVGGNGKIDFNEFTSATMHNKTEKEDHLWAFMHFDNSGYIT 488
QY 422 DELQASCTEFGICLTPIDMDIKEIDLNDGKIDPSEFTAMMRKGD-GVGRSRTMMK 476
DQ 489 DELOEAMKNGMDPETIQEIISEVDTDNGRIDYDEFFVAMMRKGNPGAENGSTYVK 545
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AAG31159
ID AAG31159 standard; Protein; 408 AA.

PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139456.
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PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147303.
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PR 01-SEP-1999; 99US-0151930.
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PR 04-OCT-1999; 99US-0157117.
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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

57.98;

Score 1501; DB 21; Length 463;

Best Local Similarity

61.4%;

Pred. No. 4.4e-125;

[illegible]

AA Using plant protoplast expression systems for rapidly screening
PT libraries of nucleic acids to identify gene that modulate expression of
PT target genes -

PS Examples; Fig 3B; 95pp; English.

AA The invention provides a high through-put assay for rapidly screening
CC a library of nucleic acid molecules to identify a gene product that
CC modulates expression of a gene of interest in plant protoplasts. The

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1927	74.3	463	1	US-07-951-715A-25		Sequence 25, Appl
2	1927	74.3	463	2	US-08-459-448A-25		Sequence 25, Appl
3	1927	74.3	463	3	US-08-459-595A-25		Sequence 25, Appl
4	1927	74.3	463	3	US-08-459-504B-25		Sequence 25, Appl
5	1927	74.3	463	3	US-08-459-444-25		Sequence 0, Appl
6	1927	74.3	463	4	US-09-547-422-25		Sequence 0, Appl
7	1672.5	64.5	639	4	US-09-347-801-17		Sequence 17, Appl
8	1437.5	55.4	464	1	US-07-951-715A-22		Sequence 22, Appl
9	1437.5	55.4	464	2	US-08-459-448A-22		Sequence 22, Appl
10	1437.5	55.4	464	3	US-08-459-595A-22		Sequence 22, Appl
11	1437.5	55.4	464	3	US-08-459-504B-22		Sequence 22, Appl
12	1437.5	55.4	464	3	US-08-459-444-22		Sequence 0, Appl
13	1437.5	55.4	464	4	US-09-547-422-22		Sequence 0, Appl
14	1277.5	49.3	408	1	US-07-951-715A-21		Sequence 21, Appl
15	1277.5	49.3	408	2	US-08-459-448A-21		Sequence 21, Appl
16	1277.5	49.3	408	3	US-08-459-595A-21		Sequence 21, Appl
17	1277.5	49.3	408	3	US-08-459-504B-21		Sequence 21, Appl
18	1277.5	49.3	408	3	US-08-459-444-21		Sequence 21, Appl
19	1277.5	49.3	408	4	US-09-547-422-21		Sequence 21, Appl
20	829	32.0	623	4	US-09-347-801-4		Sequence 4, Appl
21	826	31.9	625	4	US-09-347-801-18		Sequence 18, Appl
22	800	30.9	576	4	US-09-347-801-19		Sequence 19, Appl
23	771.5	29.8	456	1	US-08-464-164-2		Sequence 2, Appl
24	771.5	29.8	456	1	US-08-338-057-2		Sequence 2, Appl
25	771.5	29.8	456	2	US-08-668-416-2		Sequence 2, Appl
26	622	24.0	520	4	US-09-257-825B-20		Sequence 20, Appl
27	587.5	22.7	370	2	US-08-878-989-19		Sequence 19, Appl

INFORMATION FOR SEQ ID NO: 25;
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-07-951-715A-25

Query Match 74.3%; Score 1927; DB 1; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPQTPLRDLHYLLGKLGQGFQGTIVLCTEKSSTANYACKSIPKRLKLVCREDEDYVWR 73
DB 1 VLPQRTQNIREVYEVGRKLGQGFQGTTECTRRASGKFEACKSIPKRLCKEDYVWR 60
QY 74 ETQIMHLSHPNVVRIKGTEDSVFVHVMVCEGGLFDRIVSKGHFSEREAVKLKLT 133
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DB 121 IVEVVEACHSLGVMDLKPENFLDITDIDAKLKATDGLSVFYKPGESFCDDVVGSPYY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETSGIFRQILQKLFKSPDPWPTI 253
DB 181 VAPEVLKLYGPESDWSAGVILYILLSGVPPFWAETSGIFRQILQKLFKSPDPWPTI 240
QY 254 SPAADLIYKMLERSPKKRISAEALCHPWIVDEQAADPKLPDPAVLSRLKQFSQMNKIK 313
DB 241 SDSAKDLIRKMLDQNPKTRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSQMNKIK 300
QY 314 KNALRVIAERLSEBEIGGLKELFKMIDTNSGTITFEELKAGLRVSGELMESEIKSLMD 373
DB 301 KNALRVIAERLSEBEIGGLKELFKMIDTNSGTITFEELKAGLRVSGELMESEIKSLMD 360
QY 374 AADINSGTIDYGEFLATLHNKWEREILVAASDFDKGSGYITIDELQASCTEFLG 433
DB 361 AADIDKSGTIDYGEFLATVHLNKLREENLVSAFSDKSGYITIDELQACKDFGL 420
QY 434 CDTPLDDMIKEDLDNDGKIDFSEFTAMMKGD-GVGRSRTMMK 476
DB 421 DDHIDDDMIKEDLDNDGQIDYGEFAAMMKKGGIGLR-RTMRK 463

RESULT 2
US-08-459-448A-25
Sequence 25, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-448A-25

Query Match 74.3%; Score 1927; DB 2; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPQTPLRDLHYLLGKLGQGFQGTIVLCTEKSSTANYACKSIPKRLKLVCREDEDYVWR 73
DB 1 VLPQRTQNIREVYEVGRKLGQGFQGTTECTRRASGKFEACKSIPKRLCKEDYVWR 60
QY 74 ETQIMHLSHPNVVRIKGTEDSVFVHVMVCEGGLFDRIVSKGHFSEREAVKLKLT 133
DB 61 ETQIMHLSHANVVRIEGTEDSTAVHLVMELCGEGELFDRIVQKGYHSEQAARLKT 120
QY 134 ILGVVEACHSLGVMDLKPENFLPDSKDDAKLKATDGLSVFYKPGQYLDVVGSPYY 193
DB 121 IVEVVEACHSLGVMDLKPENFLDITDIDAKLKATDGLSVFYKPGESFCDDVVGSPYY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETSGIFRQILQKLFKSPDPWPTI 253
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Db 361 AADIDKSGTIDYGEFLAATVHLKLEREENLVSAFSYFDKDGSGYITIDELQOACKDFGL 420
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Db 421 DDHIDDMIKEDQNDGQIDYGEFAAMMRKGGIGR-RTMRK 463
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RESULT 3

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US-08-459-595A-25
; Sequence 25, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; OTHER INFORMATION: /note= "protein sequence for
; OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-595A-25
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Query Match 74.3%; Score 1927; DB 3; Length 463;

Best Local Similarity 78.7%; Pred. No. 1e-152;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

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QY 14 VLPYOTPRLDHYLLGKLGQGGQFTTYLCTEKSYSANYACKSIKPKLVCRDEYDVR 73
Db 1 VLPQRTQNTIREYVEYGRKLGQGGQFTTCTRRASGGKFAKSIKPKLLCKEDYDVR 60
QY 74 EIQIMHLSHPNVVRKGTEDSVFVHTVMEVCGEGGLFDRIVKGFHSEAEVKKLKT 133
Db 61 EIQIMHLSHPNVVRKGTEDSVFVHTVMEVCGEGGLFDRIVKGFHSEAEVKKLKT 120
QY 134 ILGVVEACHSLGVHRLDKPENFLFSDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVHRLDKPENFLFDTTDEDAKLKATDFGLSVFYKPGESFCDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIPRQILQGLDKSPDPWPTI 253
Db 181 VAPEVLRKLYGPESDVWSAGVILYLLSGVPPFWAETSGIPRQILQGLDKSPDPWPTI 240
QY 254 SEAAKDLVYKMLERSPKKRISAHEALCHPWIVDEQAAAPKPLDPAVLRLKQFSOMNKK 313
Db 241 SDSAKDLRLKMLDQPKRLTAHEVLRHPWIVDDIADPKLDSAVLSRLKQFSOMNKK 300
QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVSSELMSEIKSLMD 373
Db 301 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFDELKQGLKRVGSELMSEIKDLMD 360
QY 374 AADIDNSGTIDYGEFLAATLHMKNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEGL 433
Db 361 AADIDKSGTIDYGEFLAATVHLKLEREENLVSAFSYFDKDGSGYITIDELQOACKDFGL 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRRTMK 476
Db 421 DDHIDDMIKEDQNDGQIDYGEFAAMMRKGGIGR-RTMRK 463
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RESULT 4

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US-08-459-504B-25
; Sequence 25, Application US/08459504B
; Patent No. 6075185
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GENERAL INFORMATION:

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; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cortwallis Road
; CITY: Research Triangle Park
```

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? STATE: NC
? COUNTRY: USA
? ZIP: 27709
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/459,504B
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/459,595
? FILING DATE: 02-JUN-1995
? APPLICATION NUMBER: US 07/951,715
? FILING DATE: 25-SEP-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/772,027
? FILING DATE: 04-OCT-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Meigs, J. Timothy
? REGISTRATION NUMBER: 38,241
? REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (919)541-8587
? TELEFAX: (919)541-8689
? INFORMATION FOR SEQ ID NO: 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 463 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? MOLECULE TYPE: protein
? HYPOTHETICAL: NO
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..463
? OTHER INFORMATION: /note= "protein sequence for
? soybean CDPK as shown in Figure 34."
?
? US-08-459-504B-25
?
? Query Match 74.3%; Score 1927; DB 3; Length 463;
? Best Local Similarity 78.7%; Pred. No. 1e-152;
? Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
?
? Qy 14 VLPYQTPLRDLHYLLGKKGQGGFTTYLCTEKSTSANYSACKIPKRLKVCREDYEDVWR 73
? Db 1 VLPQTQIREYIEVGRKLGQGGFTTCTECTRRASGGKFAKSIPIKRLKCKEDYEDVWR 60
?
? Qy 74 EIQIMHHLSEHPNVRIKGTVEDSVFVHIVMEVCEGGELFDRIVSKGHFSREAVKLTKT 133
? Db 61 EIQIMHHLSEHANVRIEGTVEDSTAVHLVMEVCEGGELFDRIVKQGHYSERQARLTKT 120
?
? Qy 134 ILGVVEACHSLGVMRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
? Db 121 IVEVVEACHSLGVMRDLKPNFLDTTDEDAKLKATDFGLSVFYKPGSECDVVGSPYY 180
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? Qy 194 VAPEVLKCYGPEIDVNSAGVILYLLSGVPPFNAETSGIFRQILQCKLDFKSDPWPPTI 253
? Db 181 VAPEVLRLKLYGPESDVSAGVILYLLSGVPPFNAETSGIFRQILKGLKDFHSEPPWPSI 240
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? Qy 254 SEAAKDLIYKMLERSPKKRSIAHEALCPWIVDEQAAPDKPLDPVLSRLKQFSOMNKKIK 313
? Db 241 SDSAKDLIRKMLDQPKTRFLTAHEVLRHPWVDNDIAPDKPLDSAVLSRLKQFSAMNKKL 300
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? Qy 314 KMLRVIAERLSEEBEIGGLKELFKMIDRNSGTITFEELKAGLRVSGELMESETKSLMD 373
? Db 301 KMLRVIAERLSEEBEIGGLKELFKMIDRNSGTITFEELKAGLRVSGELMESETKSLMD 360
?
? Qy 374 AADINSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSGYITIDELQSACTEFLG 433
? Db 361 AADIDKSGTIDYGEFLAATVHLNKLREENLVSAFSDFDKDGSGYITIDELQACKDRGL 420
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Qy 434 CDIFLDDMIKEDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDIIHDDMIKEDLDNDGQIDYGEFAAMRRKGGIGR-RTMRK 463

RESULT 5
US-08-459-444-25
Sequence 0, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauais, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cordwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "protein sequence for
soybean CDPK as shown in Figure 34."
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
soybean CDPK as shown in Figure 34."
US-08-459-444-25

Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

Qy 14 VLPYQTPLRDLHYLLGKKGQGGFTTYLCTEKSTSANYSACKIPKRLKVCREDYEDVWR 73
Db 1 VLPQTQIREYIEVGRKLGQGGFTTCTECTRRASGGKFAKSIPIKRLKCKEDYEDVWR 60

Qy 74 EIQIMHHLSEHPNVRIKGTVEDSVFVHIVMEVCEGGELFDRIVSKGHFSREAVKLTKT 133
Db 61 EIQIMHHLSEHANVRIEGTVEDSTAVHLVMEVCEGGELFDRIVKQGHYSERQARLTKT 120

Qy 134 ILGVVEACHSLGVMRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVMRDLKPNFLDTTDEDAKLKATDFGLSVFYKPGSECDVVGSPYY 180

Qy 194 VAPEVLKCYGPEIDVNSAGVILYLLSGVPPFNAETSGIFRQILQCKLDFKSDPWPPTI 253
Db 181 VAPEVLRLKLYGPESDVSAGVILYLLSGVPPFNAETSGIFRQILKGLKDFHSEPPWPSI 240

Qy 254 SEAAKDLIYKMLERSPKKRSIAHEALCPWIVDEQAAPDKPLDPVLSRLKQFSOMNKKIK 313
Db 241 SDSAKDLIRKMLDQPKTRFLTAHEVLRHPWVDNDIAPDKPLDSAVLSRLKQFSAMNKKL 300

Qy 314 KMLRVIAERLSEEBEIGGLKELFKMIDRNSGTITFEELKAGLRVSGELMESETKSLMD 373
Db 301 KMLRVIAERLSEEBEIGGLKELFKMIDRNSGTITFEELKAGLRVSGELMESETKSLMD 360

Qy 374 AADINSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSGYITIDELQSACTEFLG 433
Db 361 AADIDKSGTIDYGEFLAATVHLNKLREENLVSAFSDFDKDGSGYITIDELQACKDRGL 420

Db 1 VLPQRTNIRVYEVGKLGQGGTTECTRRASGKGFACKSIPKRLKCKEDYDVR 60
QY 74 EIQIMHLSHPNVVRIKGTEDSVFVHVMVEGEGSELDRIYVSKGHFSREAVKLK 133
Db 61 EIQIMHLSHPNVVRIKGTEDSVFVHVMVEGEGSELDRIYVSKGHFSREAVKLK 120
QY 134 ILGVVEACHSLGVHMDLKPENFLDSDAKLAKATDGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVHMDLKPENFLDSDAKLAKATDGLSVFYKPGQYLYDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLFKSDPWP 253
Db 161 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLFKSDPWP 240
QY 254 SEAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAADPKLDPVLSRLKQFSOMN 313
Db 241 SDSAKDLIRKMLDQNPRTLAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSOMN 300
QY 314 KMLRVIAERLSEETIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELSKSLMD 373
Db 301 KMLRVIAERLSEETIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELSKSLMD 360
QY 374 AADIDNSGTIDYGEFLAATLHNMKMERELVAAFSDFDKGSGYITIDELQSACTE 433
Db 361 AADIDNSGTIDYGEFLAATLHNMKMERELVAAFSDFDKGSGYITIDELQSACTE 420
QY 434 CDTPLDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 463

RESULT 6

US-09-547-422-25
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nallini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Werlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:

RESULT 7

US-09-347-801-17
; Sequence 17, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97

; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-547-422-25
Query Match 74.3%; Score 1927; DB 4; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPQRTNIRVYEVGKLGQGGTTECTRRASGKGFACKSIPKRLKCKEDYDVR 73
Db 1 VLPQRTNIRVYEVGKLGQGGTTECTRRASGKGFACKSIPKRLKCKEDYDVR 60
QY 74 EIQIMHLSHPNVVRIKGTEDSVFVHVMVEGEGSELDRIYVSKGHFSREAVKLK 133
Db 61 EIQIMHLSHPNVVRIKGTEDSVFVHVMVEGEGSELDRIYVSKGHFSREAVKLK 120
QY 134 ILGVVEACHSLGVHMDLKPENFLDSDAKLAKATDGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVHMDLKPENFLDSDAKLAKATDGLSVFYKPGQYLYDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLFKSDPWP 253
Db 161 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLFKSDPWP 240
QY 254 SEAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAADPKLDPVLSRLKQFSOMN 313
Db 241 SDSAKDLIRKMLDQNPRTLAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSOMN 300
QY 314 KMLRVIAERLSEETIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELSKSLMD 373
Db 301 KMLRVIAERLSEETIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELSKSLMD 360
QY 374 AADIDNSGTIDYGEFLAATLHNMKMERELVAAFSDFDKGSGYITIDELQSACTE 433
Db 361 AADIDNSGTIDYGEFLAATLHNMKMERELVAAFSDFDKGSGYITIDELQSACTE 420
QY 434 CDTPLDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 463

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; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-347-801-17

Query Match          64.5%; Score 1672.5; DB 4; Length 639;
Best Local Similarity 66.2%; Pred. No. 2.6e-131;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

QY 5 PNPR-RPS-----NTVLPQYPRLRDHYLLGKLGQGGFGTGYLTCTKSTKSANY 52
Db 120 PSPPRPQVKKRVSSAGLLGSLVLRKKTENLKDKYSLGRLLGQGGFGTGLTCTKSTK 179
QY 53 AKSIPKRLVCRDYEVDVREIQIMHLSLHSEHPNVVRIKGTYESVPHVIMVECEGEL 112
Db 180 ACKSILKRLGSDDDVEDVREIQIMHLSLHSEHPNVVRIKGTYESVPHVIMVECEGEL 239
QY 113 FDRIVSGHFSEREAVALIKITLGVWEACHSLGVHMDLKPENFLDPSKDDAKLKATDF 172
Db 240 FDRIVRGHTERKAELARVIVGVVACHSGVHMDLKPENFLDPSKDDAKLKATDF 299
QY 173 GLSVFYKPGQYLDVVGSPYYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETES 232
Db 300 GLSIFFRPGQIFTDVVGSPYYVAPEVLKCYGPEADVMSAGVILYLLSGVPPFWAENQ 359
QY 233 GIPQILOGKLDKSDPWPISAEAKOLYIMLERSPKRLISAHEALCHPWIVDEQAPD 292
Db 360 GIFBEVLHGRIDFESFPWPSISDGAOKDLVRMLVRDPRKRLTAHEVLRHPWVQGVGAPD 419
QY 293 KPLDPVAVLSRLKQPSOMNKKKMLRALYIAERLSPEEIGGLKELFKMTDTONSGTITPEEL 352
Db 420 RPLDSAVLSRMKQPSAMNKKKMLRALYIAENLSEDETAGLREMEKMDADNSGOITPEEL 479
QY 353 KAGLKRVGSELMSEIKSLMDAADINSGTIDYGEFTLAATHLMKMEREEILYVAADFSD 412
Db 480 KVGLEKYGANLQSEIEYALMQAADVNDNGTIDYGEFTLAATHLMKMEREDHLFAAFQVD 539
QY 413 KDGSGYITIDLOQACFEGLCDPLDMDIKEDIDNDGKIDFSEFTAMMKRGDGVGRSR 472
Db 540 KDGSGYITADELVQACEFGLGDVQLEDLGEVDQDNDGRIDYNEFTVAMMKQ-PTVGGSR 598

RESULT 8
us-07-951-715A-22
; Sequence 22, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
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; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
; US-07-951-715A-22

Query Match          55.4%; Score 1437.5; DB 1; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRDHVLLGKLGQGGFGTGYLTCTKSTKSANYACKSIPKRLVCRDYEVDVREIQIMHHL 81
Db 9 VRAVYSMKGELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAHEDVDDVRREVQIMHHL 68
QY 82 SEHPNVVRIKGTYESVPHVIMVECEGGLFDRIVSGHFSEREAVALIKITLVGYEAC 141
Db 69 SCQPNVVGRLCAYEDKQSVHLYMELCAGGELFDRLIARGQYTERGAELRLAIQIVHTC 128
QY 142 HSLGVHMDLKPENFLDPSKDDAKLKATDFGLSVFYKPGQYLDVVGSPYYVAPEVLK 201
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Db 189 KYGPEADVMSAGVILYLLSGVPPFWAENSGIFTALRGQDLSSEFPWHPISGAKDLV 248
QY 262 YKMLERSPKRLISAHEALCHPWIVDEQAPDPLDPAVLSRLKQPSOMNKKKMLRALYIA 321
Db 249 KKMLNINPKERLTAFQVNLNHPWIKEDGADPTPLDNNVLDRLKQFRAMNQFKKAALRIA 308
QY 322 ERLSEERIGGLKELFKMTDTONSGTITFEELKAGLKRVGSELMSEIKSLMDAADINSG 381
Db 309 GCLSEERIGGLKELFKMTDTONSGTITDELKHLGKLVGSELMSEIKSLMDAADINSG 368
QY 382 TIDYGEFTLAATHLMKMEREEILYVAADFSDPKDGSYITIDELQASCTEFGICDT-PLDD 440
Db 369 LIDDEFVTAIVHNMKLDREHLYTAFQYFDKDNKSQYITKEELEHALKEQGLYDADKID 428
QY 441 MIKEIDLNDGKIDFSEFTAMMKRG 465
Db 429 IISDADSDNDGRIDYSEFVAMMKRG 453

RESULT 9
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US-08-459-448A-22
; Sequence 22, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 601810artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22
Query Match 55.4%; Score 1437.5; DB 2; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
22 LRDIYLLGKLGQGGFTTILCTEKSTKSANYACKSIPKRLVCRDYEDYWRRLQIMHHL 81

Db 9 VRATYSMGKELRGQFGVTHLCTHRTSGEKLACKTIAKRLAARDVDDVRRREVQIMHHL 68
QY 82 SEHPNVRIRKGYEDSVFVHIVMEVCEGGEFLFDRIYVSKGHFSREAVKLIKTLIGVVEAC 141
Db 69 SGQPNVGLRGAYEDKQSVHVLVMELCAGGELFDRIIARQYITRGAELRLAIVQIVHTC 128
QY 142 HSLGVMRDLKPNFLFDSPKDAKDKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 201
Db 129 HSMGVMRDLKPNFLFDSKDEDAPLKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 188
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRILQKLDKFDSDPPTTSEAKDLI 261
Db 189 KYGPEADINSGVYMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPPHISPGAKDLV 248
QY 262 YKMLERSPKKRISAHEALCHPWIVDQAAAPDKPLDPAVLRLKOFKOFOMKIKMALRVIA 321
Db 249 KMLNINPKRLTAFOVLNHPWIKEDGADPTPLDNNVLDRLKQFRAMNQFKAAALRIIA 308
QY 322 ERLSEEEIGLKFELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLMDAADIDNSG 381
Db 309 GCLSEBEITGLKEMFNKIDKNSGTTTLDLKHGLAKHGPKLSDSEMEKIMEAADADGNG 368
QY 382 TDYGEFLAATLHMKNKEREELVAAFSDFDKDGSYITIDELOSACTEGLCDT-PLDD 440
Db 369 LIDYDEFVTATVHMKNLDRHEHLYTAFQYFDKNSGYITKEELEHALKEGGLYDADKIND 428
QY 441 MIKEIDLNDGKIDFSEFTAMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMRKG 453

RESULT 10
US-08-459-595A-22
; Sequence 22, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 601810artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/951,715
;; FILING DATE: 25-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/772,027
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pace, Gary M.
;; REGISTRATION NUMBER: 40403
;; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8582
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 464 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..464
;; OTHER INFORMATION: /note= "derived protein sequence of
US-08-459-595A-22 pollen specific CDPK as disclosed in Figure 34."

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
QY 22 LRDHLLGKKGQGGTGYLCTEKSTANYACKSPKRLVCRDYEDVWREIOMHHL 81
DB 9 VRATYSMGKELGQGVTHCTHRTSGEKLAKTAKRLAAREDDVDVREVQIMHHL 68
QY 82 SEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLITILGVVEAC 141
DB 69 SQGPNNVGLRGAYEDKQSVHLMELCAGGELEFDRIIARQYTERGAELLRAIVQIVHTC 128
QY 142 HSLGVNHRDLKPFENLFDSPKDKALKATDFGLSVFKPGQVLYDVVGSPIYVAPVLAK 201
DB 129 HSMGVNHRDIPENFLLSKEDAPLAKATDFGLSVFKPGQVLYDVVGSPIYVAPVLAK 188
QY 202 CYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRILQGLDKFSDPWPPTISEAAKDLI 261
DB 189 KYGPEADVWSGVMLYIFLAGVPPWAENENGIFTAILRGQLDLSSEPPHISPGAKDLV 248
QY 262 KYMLSPKPKRISAEHALCPHWIVDEQAPDPLDPAVLSRLKQFSQMKIKKMAURVTA 321
DB 249 KMLNINPKERTAFQVNEHPWIKEDGDADPTPLDNVVDRLKQFRAMNQFKKALRIIA 308
QY 322 ERLSEIEIGLKFELKMIIDTNSGTITFEELKAGLKRVSSELMESIKSLMDAADIDNSG 381
DB 309 GCLSEIEITGLKEMFNIDKNSGTITLDELKHLAKHGFKLSDSMEKLMRAADADGNG 368
QY 382 TIDYGEFLAATLHMKNREELVIAFSDFDKDGSGYITIDELQSACTEFLGCDT-PLDD 440
DB 369 LIDYDFVATVHMKNLDRHEHLYTAFQYFDKNSGYITKEELHALKQGLYDADKID 428
QY 441 MIKEIDLNDGKIDSEFFAMRKG 465
DB 429 IISDADSDNDGRIDYSEFVAMRKG 453

RESULT 11

US-08-459-504B-22
; Sequence 22, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.

;; APPLICANT: Kramer, Vance C.
;; APPLICANT: Warren, Gregory W.
;; APPLICANT: Evola, Stephen V.
;; APPLICANT: Crossland, Lyle D.
;; APPLICANT: Wright, Martha S.
;; APPLICANT: Merlin, Ellis J.
;; APPLICANT: Launis, Karen L.
;; APPLICANT: Rothstein, Steven J.
;; APPLICANT: Bowman, Cindy G.
;; APPLICANT: Dawson, John L.
;; APPLICANT: Dunder, Erik M.
;; APPLICANT: Pace, Gary M.
;; APPLICANT: Suttie, Janet L.
;; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;; NUMBER OF SEQUENCES: 94
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 6075185artis Corporation
;; STREET: 3054 Cornwallis Road
;; CITY: Research Triangle Park
;; STATE: NC
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,504B
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/459,595
;; FILING DATE: 02-JUN-1995
;; APPLICATION NUMBER: US 07/951,715
;; FILING DATE: 25-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/772,027
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8587
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 464 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..464
;; OTHER INFORMATION: /note= "derived protein sequence of
US-08-459-504B-22 pollen specific CDPK as disclosed in Figure 34."

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
QY 22 LRDHLLGKKGQGGTGYLCTEKSTANYACKSPKRLVCRDYEDVWREIOMHHL 81
DB 9 VRATYSMGKELGQGVTHCTHRTSGEKLAKTAKRLAAREDDVDVREVQIMHHL 68
QY 82 SEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLITILGVVEAC 141
DB 69 SQGPNNVGLRGAYEDKQSVHLMELCAGGELEFDRIIARQYTERGAELLRAIVQIVHTC 128

QY 142 HSLGVHRLKPNELPDSKDAKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 201
Db 129 HSMGVHRDLKPNELPDSKDAKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 188
QY 202 CYGPEIDVWSAGVILXILSVPFPFAETSGIFRQILOGLKDFKSDPWPPTISEAAKDLI 261
Db 189 KYGPEADINSVGMVLIYFLAGVPPFAENENGIFTALRGQLDLSSEPHISPGAKDLV 248
QY 262 YKMLSPKKRISAEALCHPWIVDQQAAPDKPLDPAVLRLKQFQOMNKKMALRVIA 321
Db 249 KKMNLNPKERLTAQVNLHPWKEDGADPTPLDNNVLDRLKQFRAMNQFKAALRIIA 308
QY 322 ERLSEEBIGLKEFELKPMIDTNSGTITFEELKAGLKVGSSELMSESETKSLMDADIDNSG 381
Db 309 GCLSEEBITGLKEMFNIDKNSGTITLDELKHLGAKHGPKLSDSEMEKLEAADADGNG 368
QY 382 TIDYGEFLAATLHMNMKMEREEILVAAFSDFDKDGSYITIDELQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFTVATVHMNKLDRHEHLYTAQYFDKNSGYITKEELEHALKEOGLYADADKIKD 428
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 12

US-08-459-444-22
; Sequence 0, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalin M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-Sep-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-Oct-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of

; pollen specific CDPK as disclosed in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-459-444-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
QY 22 LRHYLLGKLGKGGFGTTVLCCTEKTSTANYACKSPKRLKVCREDYEDVYREIQIMHHL 81
Db 9 VRATYSMGKELGRGQFVTHLCTHRTSGEKLACKTIARKLAAEDVDVRRVQIMHHL 68
QY 82 SEHPNVVRIKGTYESVYFVHVMVEVCGGELFDRIVSKGHSEFSEAEVAKLIKTILGVVEAC 141
Db 69 SGQPNVVGLRGAYEDKQSVHVMELCAGGELFDRIIARGQYTERGAELRLRAIVQIVTC 128
QY 142 HSLGVHRLKPNELPDSKDAKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 201
Db 129 HSMGVHRDLKPNELPDSKDAKATDFGLSVFKPGQYLYDVVGSPPYVAPVLLK 188
QY 202 CYGPEIDVWSAGVILXILSVPFPFAETSGIFRQILOGLKDFKSDPWPPTISEAAKDLI 261
Db 189 KYGPEADINSVGMVLIYFLAGVPPFAENENGIFTALRGQLDLSSEPHISPGAKDLV 248
QY 262 YKMLSPKKRISAEALCHPWIVDQQAAPDKPLDPAVLRLKQFQOMNKKMALRVIA 321
Db 249 KKMNLNPKERLTAQVNLHPWKEDGADPTPLDNNVLDRLKQFRAMNQFKAALRIIA 308
QY 322 ERLSEEBIGLKEFELKPMIDTNSGTITFEELKAGLKVGSSELMSESETKSLMDADIDNSG 381
Db 309 GCLSEEBITGLKEMFNIDKNSGTITLDELKHLGAKHGPKLSDSEMEKLEAADADGNG 368
QY 382 TIDYGEFLAATLHMNMKMEREEILVAAFSDFDKDGSYITIDELQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFTVATVHMNKLDRHEHLYTAQYFDKNSGYITKEELEHALKEOGLYADADKIKD 428
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 13

US-09-547-422-22
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalin M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park

```
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/547,422
  FILING DATE: 11-Apr-2000
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/459,595
  FILING DATE: 02-JUN-1995
  APPLICATION NUMBER: US 07/951,715
  FILING DATE: 25-SEP-1992
  APPLICATION NUMBER: US 07/772,027
  FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Melgs, J. Timothy
  REGISTRATION NUMBER: 38,241
  REFERENCE/DOCKET NUMBER: S-18805H
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (919)541-8587
    TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7 note= "derived protein sequence of
pollen specific CDPK as disclosed in Figure 34."
SEQUENCE CHARACTERISTICS:
  LENGTH: 464 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  HYPOTHETICAL: NO
  FEATURE:
    NAME/KEY: Protein
    LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-547-422-22

Query Match      55.4%; Score 1437.5; DB 4; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRDHLLGKLGQGFYTLCTEKSTSNYACKSTPKKLVKCYREDYDVWREIQIMHHL 81
Db 9 VRATYMGKELGQGFVTHLCTHRTSGKFLACKTTAKRKLAAREDVDVREVQIMHHL 68
QY 82 SEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLIKITLGVVEAC 141
Db 69 SGQPNVVGRLGAYEDKQSVHLMVCEGGELEFDRIIARQYTERGAAGELRAIVQIVHTC 128
QY 142 HSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFKPGQYLYDVVGSPPYVAPEVLKK 201
Db 129 HSGVMNHRDIKPEFNLLSKDEAPLKATDFGLSVFKEGELLROIIVGSAYVIAPEVLKR 188
QY 202 CYGPEIDVMSAGVILYLLSGVPPWAEETSGIFRILQGLKDFKSDPPTTSEAAKDLI 261
Db 189 KTGPEADIVSGVGLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHPISPGAKDIV 248
QY 262 YKMLERSPKKRISAHEALCHPWPLVDQAAAPDKPLDPAVLRSRLKQFSOMKIKKMLARVIA 321
Db 249 KKMNLNPKERLTAFOVLNHPWKEDGADPTPLDNNVLDRLKQFAMQFKKAALRIITA 308
QY 322 ERLSEIEGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMDAADIDNSG 381
Db 309 GCLSEIEITGLKEMFNIDKNSGTTTLDELKHLAKHGPKLSDSEMKLMEGAADAGNG 368
QY 382 TIDYGEFLAATLHNMKMERELVAFSDFDKSGSYIILDELOQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFTATVHMNKLDRHEEHLTYTAFQYEDKDNSGYITKEELEHALKEQGLYDADKIND 428
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QY 441 MIKEIDLDNDGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 14
US-07-951-715A-21
; Sequence 21, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/951,715A
  FILING DATE: 25-SEP-1992
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/772,027
    FILING DATE: 04-OCT-1991
  ATTORNEY/AGENT INFORMATION:
    NAME: Sprull, W. Murray
    REGISTRATION NUMBER: 32,943
    REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (919)541-8615
    TELEFAX: (919)541-8689
  INFORMATION FOR SEQ ID NO: 21:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 408 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
US-07-951-715A-21

Query Match      49.3%; Score 1277.5; DB 1; Length 408;
Best Local Similarity 61.9%; Pred. No. 1.2e-98;
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 76 QIMHHLSEHPNVVRKGYEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSEREAVKLIKITL 135
Db 1 QIMHLSGQPNVVGRLGAYEDKQSVHLMVCEGGELEFDRIIARQYTERGAAGELRAIV 60
QY 136 GYVEACHSGVMNHRDLKPNFLDPSKDDAKLKATDFGLSVFKPGQYLYDVVGSPPYVA 195
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Db 61 QIVHTCHSMGVHRDIKPFENLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYIIA 120
QY 196 PEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTISE 255
Db 121 PEVLKRYGPEADTWSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHPISP 180
QY 256 AAKDLIYKMLERSPKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKKM 315
Db 181 GAKDLVKKMLNINPKERLTAFQVLNHHWIKEDGDAPDTPLDNVVLDRLKQFRANNOFKKA 240
QY 316 ALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKRVGSELMESEIKSLMDAA 375
Db 241 ALRIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKHLGAKHGPKLSSEMEKLMEEA 300
QY 376 DIDNSGTIDYGEFLAATLHNMKWEREILVAAFSDPKDGSYITIDELQSACTEFGLCD 435
Db 301 DADGNGLIDYDEFVATVHNMKLDREHLYTAFQYFDKNSGYITKEELEHALKEQGLYD 360
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 361 ADKIKDIISDSDNDGRIDYSEFVAMMRKG 391

RESULT 15

US-08-459-448A-21
Sequence 21, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evoila, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-448A-21

Query Match 49.3%; Score 1277.5; DB 2; Length 408;

Best Local Similarity 61.9%; Pred. No. 1.2e-98;

Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 76 QIMHLSHPNVVRIKCTYEDSVHIVMEVCGEGELFDRIVSKGHSESEAVKLIKIL 135

Db 1 QIMHLSGQPNVGLRGAYEDKOSVHLVMELCAGGELFDRIIARGQYTERGAALLRAIV 60

QY 136 GVVEACHSLGVMHRDLKPFNLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVA 195

Db 61 QIVHTCHSMGVHRDIKPFENLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYIIA 120

QY 196 PEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTISE 255

Db 121 PEVLKRYGPEADTWSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHPISP 180

QY 256 AAKDLIYKMLERSPKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKKM 315

Db 181 GAKDLVKKMLNINPKERLTAFQVLNHHWIKEDGDAPDTPLDNVVLDRLKQFRANNOFKKA 240

QY 316 ALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKRVGSELMESEIKSLMDAA 375

Db 241 ALRIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKHLGAKHGPKLSSEMEKLMEEA 300

QY 376 DIDNSGTIDYGEFLAATLHNMKWEREILVAAFSDPKDGSYITIDELQSACTEFGLCD 435

Db 301 DADGNGLIDYDEFVATVHNMKLDREHLYTAFQYFDKNSGYITKEELEHALKEQGLYD 360

QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465

Db 361 ADKIKDIISDSDNDGRIDYSEFVAMMRKG 391

Search completed: March 26, 2003, 13:13:54

Job time : 28 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 13:12:27 ; Search time 118 Seconds
(without alignments)
246.341 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593
Sequence: 1 METKKNPRPSNTVLPYQTP.....KNLNFNIAAFVGDEKSD 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1927	74.3	463	9	US-09-988-462-25
2	1672.5	64.5	639	10	US-09-854-731-17
3	1509.5	58.2	549	10	US-09-828-313-39
4	1437.5	55.4	464	9	US-09-988-462-22
5	1277.5	49.3	408	9	US-09-988-462-21
6	849	32.7	597	10	US-09-828-313-38
7	829	32.0	623	10	US-09-854-731-4
8	826	31.9	625	10	US-09-854-731-18
9	800	30.9	576	10	US-09-854-731-19
10	587.5	22.7	317	9	US-09-935-464-36
11	587.5	22.7	370	9	US-10-142-356-7
12	587.5	22.7	370	10	US-09-817-181-4
13	554	21.4	357	9	US-10-024-036B-2
14	543.5	21.0	556	12	US-10-096-960-4
15	543	20.9	460	9	US-09-935-464-3
16	543	20.9	476	9	US-09-935-464-5
17	539	20.8	565	12	US-10-096-960-2
18	538.5	20.8	326	10	US-09-817-181-2
19	533.5	20.6	387	10	US-09-771-161A-188

20	530	20.4	295	9	US-09-988-462-23	Sequence 23, Appl
21	510.5	19.7	648	9	US-10-024-036B-5	Sequence 5, Appl
22	510.5	19.7	817	10	US-09-992-481-4	Sequence 4, Appl
23	501	19.3	765	9	US-10-217-357-4	Sequence 4, Appl
24	501	19.3	765	10	US-09-975-326-4	Sequence 4, Appl
25	501	19.3	766	9	US-09-934-406-2	Sequence 2, Appl
26	501	19.3	766	9	US-10-217-357-2	Sequence 2, Appl
27	501	19.3	385	9	US-10-116-332-2	Sequence 2, Appl
28	496	19.1	454	9	US-09-771-161A-238	Sequence 238, App
29	489.5	18.9	545	9	US-10-142-356-6	Sequence 6, Appl
30	473.5	18.3	543	10	US-09-740-627-1	Sequence 1, Appl
31	473	18.2	280	10	US-09-835-788A-16	Sequence 16, Appl
32	468.5	18.1	406	10	US-09-771-161A-210	Sequence 210, App
33	461.5	17.8	261	9	US-09-925-299-983	Sequence 983, App
34	460	17.7	261	10	US-09-925-299-983	Sequence 983, App
35	460	17.7	821	9	US-10-081-119-16	Sequence 16, Appl
36	459.5	17.7	740	10	US-09-771-161A-265	Sequence 265, App
37	457.5	17.6	740	10	US-09-771-161A-266	Sequence 266, App
38	457.5	17.6	522	10	US-09-740-627-11	Sequence 11, Appl
39	453	17.5	501	10	US-09-797-039-2	Sequence 2, Appl
40	447.5	17.3	501	12	US-10-153-921-2	Sequence 2, Appl
41	447.5	17.3	1518	10	US-09-801-368-152	Sequence 152, App
42	446	17.2	1203	10	US-09-799-875-5	Sequence 5, Appl
43	445.5	17.2	514	10	US-09-922-138-5	Sequence 5, Appl
44	443	17.1	514	10	US-09-841-683-2	Sequence 2, Appl
45	443	17.1				

ALIGNMENTS

RESULT 1

US-09-988-462-25
; Sequence 25, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen I.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 5054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
soybean CDPK as shown in Figure 34."
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-988-462-25

Query Match 74.3%; Score 1927; DB 9; Length 463;
Best Local Similarity 78.7%; Pred. No. 2.9e-128;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPTQTPRLRDHYLLKGLGQGFQGTTLCTEKSISANYACKSIPKRLKLVCHREDYEDVWR 73
Db 1 VLPTQTPRLRDHYLLKGLGQGFQGTTLCTEKSISANYACKSIPKRLKLVCHREDYEDVWR 60
QY 74 EIQIMHLSSEHPNVRIKGTIEDSVFVHVMVEVCGEGELFDRIVSKGHFSEREAVKLIKT 133
Db 61 EIQIMHLSSEHPNVRIKGTIEDSVFVHVMVEVCGEGELFDRIVSKGHFSEREAVKLIKT 120
QY 134 ILGVVEACHSLGVMHRLDKPENFLDSPKDDAKLKAIDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVMHRLDKPENFLDSPKDDAKLKAIDFGLSVFYKPGQYLYDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWSAGVYLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTI 253
Db 181 VAPEVLKCYGPEIDVWSAGVYLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTI 240
QY 254 SEAAKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAYISRLKQFSOMNKK 313
Db 241 SDSAKDLIRKMLDQNPKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSOMNKK 300
QY 314 KVALRVIAERLSEETIGGLKELFKMTDTSNCTITFEELKAGLKRVSGLMESEIKSLMD 373
Db 301 KVALRVIAERLSEETIGGLKELFKMTDTSNCTITFEELKAGLKRVSGLMESEIKSLMD 360
QY 374 AADINSGPIDYGEFLAATPLHNKMEREBILVAAFSDPKDGSYITITDELQSACTEFLG 433
Db 361 AADIDKSGTIDYGEFLAATPLHNKMEREBILVAAFSDPKDGSYITITDELQSACTEFLG 420
QY 434 CDTPLDDMIKEIDLDNDGKIDFSEPTAMRKGD-VGVRSTMMK 476
Db 421 DDHIDDMIKEDQDNDGQIDYGEFAAMRKGGTIGR-RTMRK 463

RESULT 2
US-09-854-731-17
; Sequence 17, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438

; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-17

Query Match 64.5%; Score 1672.5; DB 10; Length 639;
Best Local Similarity 66.2%; Pred. No. 3.6e-110;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

QY 5 PNPR-RPS-----NTVLPYQTPRLRDHYLLKGLGQGFQGTTLCTEKSISANY 52
Db 120 PPSRPRQVKRYSSAGLLLSGLVLRKTKENLKDYSGLRRLGQGFQGTTHLCVERATGKEL 179
QY 53 ACKSIPKRLKLVCHREDYEDVWREIQIMHLSSEHPNVRIKGTIEDSVFVHVMVEVCGEL 112
Db 180 ACKSILKRLKLGSDDDVEDVRREIQIMHLSSEHPNVRIKGTIEDSVFVHVMVEVCGEL 239
QY 113 FDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRLDKPENFLDSPKDDAKLKAIDF 172
Db 240 FDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRLDKPENFLDSPKDDAKLKAIDF 299
QY 173 GLSVFYKPGQYLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTI 232
Db 300 GLSVFYKPGQYLYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPPTI 359
QY 233 GTFRIQLQGLDFKSDPWPPTI SEAAKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPD 292
Db 360 GTFEEVLHGRLEDFSEPPWPSISDGAKDLVRRMLVRDPKRLTAHEVLRHPWVQVGVAPD 419
QY 293 KPLDPAVLISRLKQFSOMNKKIKKALRVIAERLSEETIGGLKELFKMTDTSNCTITFEEL 352
Db 420 RPLDPAVLISRLKQFSOMNKKIKKALRVIAERLSEETIGGLKELFKMTDTSNCTITFEEL 479
QY 353 KAGLRVSELSMESIKSLMDAADINSGTIDYGEFLAATPLHNKMEREBILVAAFSDPD 412
Db 480 KVLGKLVGANLQSEBIYALMAQADVNDNGTIDYGEFLAATPLHNKMEREBILVAAFSDPD 539
QY 413 KDGSGYITITDELQSACTEFLGCDTFLDDMIKEIDLDNDGKIDFSEPTAMRKGDVGVRSR 472
Db 540 KDGSGYITITDELQSACTEFLGCDTFLDDMIKEIDLDNDGKIDFSEPTAMRKGDVGVRSR 598

RESULT 3
US-09-828-313-39
; Sequence 39, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-39

Query Match 58.2%; Score 1509.5; DB 10; Length 549;
Best Local Similarity 60.8%; Pred. No. 9.1e-99;

Matches 290: Conservative 70: Mismatches 112: Indels 5: Gaps 3:

QY 5 PNPRESNT---VLEPTQPLRLDHYLKKLGQGGFTYLCSTKSTANYACKSIPKRR 61
Db 69 PRPKPASRSVSGVLKPLSDIRQSYILGRELGRGQFGVYLTCTDKMTNEAYACKSIARRK 128
QY 62 IVCREDYEDVWEIOIMHLSHPNNVRIKGYDSVFIHVMVECEGELFDRIVSKGH 121
Db 129 LFSKEDIEDVKEVQIMHLSGTPNIVLVKDFEDKHSVHLVWELCAGGELFDRIIAIGH 188
QY 122 FSEREAVALIKLIGVWEACHSLGVMHDLKPEFLSPKDDAKLKATDFGLSVFYKPG 181
Db 189 YSERAADMCVRVIVVHCHSLGVMHDLKPEFLSPKDDAKLKATDFGLSVFYKPG 248
QY 182 QYLDVWGSPPYVAPEVLKCKYKPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 241
Db 249 DVFQIVGSAYVAPEVLKCKYKPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 308
QY 242 KLDKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDPPLPAVL 301
Db 309 HLDENDPMPKISNGAKDLVRKMLPNVKIRLTAQVLMHPMKEDGADVPFLDNAVIT 368
QY 302 RLKQFSQNMKIKMALRVIAERLSEEEIGGLKELFKMIDTNSGTITPEELKAGLKRVGS 361
Db 369 RLKNSAANKMKALKVIAESLSEEEIVGLREMPKSIDTNSGIVTPEELKAGLKRVGS 428
QY 362 ELWSEIKSLMDAADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKDGSYITI 421
Db 429 KLNESDIRKLEAADVGNKIDFNEFISATMNMKTEKEDHLWAFMHFDFTDNGSYITI 488
QY 422 DELQACTEFGLCD-TPDDMTKEITDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 489 DELQAMEKMGSDPETIQEIISEVTDNDGRIDYDFVMMRKNKGNPGAENGTVNK 545

RESULT 4

US-09-988-462-22
; Sequence 22, Application US/09988462
; Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESS: Sygenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NOV-98
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
pollen specific CDPK as disclosed in Figure 34."
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-988-462-22

Query Match 55.4%; Score 1437.5; DB 9; Length 464;
Best Local Similarity 60.9%; Pred. No. 8.7e-94;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGQGGFTYLCSTKSTANYACKSIPKRRKLVCRDIEDVWVEIOIMHHL 81
Db 9 VRATYSMGKELGRGQFGVYLTCTHRTSGELKACKIAKRLAAREDDVDVREVOIMHHL 68
QY 82 SEHPNNVRIKGYDSVFIHVMVECEGELFDRIVSKGHFSEREAVALIKLIGVWEAC 141
Db 69 SQGPNNVGLRGAYEDKQSVHLMELCAGGELFDRIIAIGHVQYTERGAALLRAIVOIVHTC 128
QY 142 HSLGVMHDLKPEFLSPKDDAKLKATDFGLSVFYKPGVLYDVGVSPYVAPEVLKK 201
Db 129 HSMGVMHDLKPEFLSPKDDAKLKATDFGLSVFYKPGVLYDVGVSPYVAPEVLKK 188
QY 202 CYGEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDKSDPWTISEAAKDLI 261
Db 189 KYGPEADIVSGVILYIFLAGVPPFWAENENGIFAILRGQLDLSSEPWPSPGAKDLV 248
QY 262 YKMLERSPKKRISAHEALCHPWIVDEQAAPDPPLPAVLRLKQFSQNMKIKMALRVIA 321
Db 249 KMLNINPKERLTAFQVLMHPMKEDGADVPFLDNAVITLDRKQPMNQFKKALRIIA 308
QY 322 ERLSEEEIGGLKELFKMIDTNSGTITPEELKAGLKRVGSSELMSEIKSLMDAADINDSG 381
Db 309 GCLSEEEITGLKEMFNKIDKNSGIIITDELKHGLAKHGPKLSDSEMKLMDAADINDSG 368
QY 382 TIDYGEFLAATLHMNMEREELVAAFSDFDKDGSYITIDELQACTEFGLCD-PLDD 440
Db 369 LIDYGEFVTATVHNMKLDREHLYTAFQYFDKNSGYITKEELHAKLEOGLYDADKIKD 428
QY 441 MIKEITDLDNGKIDFSEFTAMMRKGD 465
Db 429 IISDADSNDGRIDYSEFVAMMRKGD 453

RESULT 5

US-09-988-462-21
; Sequence 21, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.

Db 538 KEGNRVYPPDEL---AKEMGLAPNPAQVFLDWIRQ-----SDGRLSFTGTKLH----- 585
QY 469 GRSTMMKNL 478
Db 586 GISSRAIKNL 595

RESULT 7
US-09-854-731-4
; Sequence 4, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-854-731-4

Query Match 32.0%; Score 829; DB 10; Length 623;
Best Local Similarity 40.6%; Pred. No. 9e-51;
Matches 183; Conservative 87; Mismatches 155; Indels 26; Gaps 11;

QY 26 YLLGKKGLOGGFGTTCYCTEKSANY-----ACKSIPKRLKVCREDYEDVWREIQIMHH 80
Db 172 YELGKEVGRGHFGHT--CSAVVKKGYKGTAVAKIIAKAKMTTATSIEDVRREVKILRA 229
QY 81 LSHPNVRIKGYEDSVFVHIYMEVCEGELFDRIYSK--GHFSEAEVKKLTKILGVVE 139
Db 230 LSGHNNLVFYDACEGDLNVIYIMELCEGELDLRLARGRYTEDEAKAIVQILSVVA 289
QY 140 ACHSLGVHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 199
Db 290 FCHLQGVVHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 349
QY 200 KKYGPEDVWSAGVLYLILSGVPPFWAETESGIFRQILQKLDKDFKSDPWTISEAAKD 259
Db 350 HRSYSMEADVWSGVITYILLCGRFPFWAETESGIFRSVLRADPNFDDSPWPTVSAEAKD 409
QY 260 LIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKKIKMALRV 319
Db 410 FVKRLNKDYKRMTAVQALTHPWLDEQR--QIPDLILIFRLIKQYLRATPKRLALKA 467
QY 320 IAEIRLSEELIGLKEFLKMDIDTNSGTITFEELKAGLRKVGSELM--ESEIKSLMDAADID 378
Db 468 LSKALREDELLYLQFKLLE--PRDGFVSLDNFRTALTRYLTDAMKRSRVLEFQHALEPL 526
QY 379 NSGTIDYGEFLAATL---HMNMKMER--EELILVAAFSDPKDGSYITIDELQSNCTEFGLC 434
Db 527 AYRMDFEFCAAATSPYQLEALERWEEIAGTAFQHFQEGNRSVISVEEL---AQELNLA 583
QY 435 DTP---LDDMIKEIDLNDGKIDFSFTAMM 462
Db 584 PTHYSIVQDWIRK---SDGKLNFLGFTKFL 610
RESULT 8
US-09-854-731-18
; Sequence 18, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming

; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match 31.9%; Score 826; DB 10; Length 625;
Best Local Similarity 40.8%; Pred. No. 1.5e-50;
Matches 183; Conservative 85; Mismatches 159; Indels 22; Gaps 10;
QY 26 YLLGKKGLOGGFGTTCYCTEKS---TSANYACKSIPKRLKVCREDYEDVWREIQIMHLS 82
Db 174 YDLGKEVGRGHFGHTCSAVVKKGEHKGHTVAVAKIIISKAKMTTATSIEDVRREVKILKALS 233
QY 83 EHPNVVRIKGYEDSVFVHIYMEVCEGELFDRIYSK--GHFSEAEVKKLTKILGVVEAC 141
Db 234 GHDLNLYRFYDACEGDLNVIYIMELCEGELDLRLARGRYTEDEAKAIIQILSVVAF 293
QY 142 HSLGVHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLK 201
Db 294 HLGQVHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLK 353
QY 202 CYGPEIDVWSAGVLYLILSGVPPFWAETESGIFRQILQKLDKDFKSDPWTISEAAKDLI 261
Db 354 SYSMEADVWSGVITYILLCGRFPFWAETESGIFRSVLRADPNFDDSPWPTVSAEAKDFV 413
QY 262 YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKKIKMALRVIA 321
Db 414 KRLNKDYKRMTAVQALTHPWLDEQR--QIPDLILIFRLVQYLRATPKRLALKALS 471
QY 322 ERUSEEIGLKEFLKMDIDTNSGTITFEELKAGLRKVGSELM--ESEIKSLMDAADIDNS 380
Db 472 KALSEDELLYLQFKLLE--PRDGFVSLDNFRTALTRYLTDAMKRSRVLEFQHALEPLAY 530
QY 381 GTIDYGEFLAATL---HMNMKMER--EELILVAAFSDPKDGSYITIDELQSNCTEFGLCDT 436
Db 531 RMDFEFCAAATSPYQLEALERWEEIAGTAFQHFQEGNRSVISVEEL---AQELNLAET 587
QY 437 P---LDDMIKEIDLNDGKIDFSFTAMM 462
Db 588 HYSIVQDWIRK---SDGKLNFLGFTKFL 612

RESULT 9
US-09-854-731-19
; Sequence 19, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-854-731-19
Query Match 30.9%; Score 800; DB 10; Length 576;

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Db    119 VKYLDLGIVHRDLKPENLLYSYLDEDSKIMISDFGLSKMEDPGSVLSTAGCTGPIVAPE 178
Qy    198 VL-KKCYPGEIDVWSAGVILYILLSGVPFPPWAETESGFRIQLCKDfKSDPWPPTISEA 256
      || :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db    179 VLAOKPSKYADVCSIGVIALLCGPPFPFYDDENDAKLFEGAILKAKEYEFDSPYWDDISDS 238
Qy    257 AKDIUYKMLESPPKKRISAHAELCHPWITVDQAAPDKPLDPAVLSRLKFQSOMNKKIK 314
      ||| :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db    239 AKDFTRHLMEXDPKRFTCEALQHHPWTAGDTAL-DKNIHOSVSSEQIKNFAKSKWKQ 295

RESULT 11
US-10-142-356-7
; Sequence 7, Application US/10142356
; Publication No. US20030036183A1
; GENERAL INFORMATION:
; APPLICANT: Boylan, John F.
; APPLICANT: Bowers, Alex J.
; TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
; FILE REFERENCE: 01017/37177A
; CURRENT APPLICATION NUMBER: US/10/142,356
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 60/290,276
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-142-356-7

Query Match          22.7% ; Score 587.5 ; DB 9 ; Length 370 ;
Best Local Similarity 41.6% ; Pred. No. 4.8e-34 ;
Matches 124 ; Conservative 55 ; Mismatches 114 ; Indels 5 ; Gaps 4 ;

Qy    18 QTPRLRHLYLGGKLGGOGFGTTVLCTEKSTSANVACKSIPKRLVCVEDYEDYVREIQI 77
      | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db    12 QAEDIRLIYDFRDVLGTGAFFSEVALAEADKRQTQKLVAIKCIAKEALEGKEG--SMENEIAV 69
      :|| :||||| :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :

Qy    78 MHHLSEHPNVVRKIPTYEDSVFVHYHVMEVCGGELFDLRIVSKGHFSEREAYVKLIAKTILGV 137
      :|| :||||| :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db    70 LHKI-KHPNIIVALDDIYESGGHLYLMLQVSGGELFDRIVEKGFEVTTERDAKSRLFQVLDA 128
      :|| :||||| :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :

Qy    138 VEACHSLGYMHRDLKPENFLFSDPKDAKLAATDFGLSFVFYKPGGYLYDVVGSPYYVAPE 197
      | :||||| :||||| :|| :||| :||| :||| :||| :||| :||| :||| :||| :
Db    129 VKYLDLGIVHRDLKPENLLYSYLDEDSKIMISDFGLSKMEDPGSVLSTAGCTGPIVAPE 188
      || :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :

Qy    198 VL-KKCYPGEIDVWSAGVILYILLSGVPFPPWAETESGFRIQLCKDfKSDPWPPTISEA 256
      || :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db    189 VLAOKPSKYADVCSIGVIALLCGPPFPFYDDENDAKLFEGAILKAKEYEFDSPYWDDISDS 248
Qy    257 AKDIUYKMLESPPKKRISAHAELCHPWITVDQAAPDKPLDPAVLSRLKFQSOMNKKIK 314
      ||| :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db    249 AKDFTRHLMEXDPKRFTCEALQHHPWTAGDTAL-DKNIHOSVSSEQIKNFAKSKWKQ 305

```

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RESULT 12
US-09-817-181-4
; Sequence 4, Application US/09817181
; Patent No. US20020142427A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001189
; CURRENT APPLICATION NUMBER: US/09/817,181
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 370

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; TYPE: PRT
 ; ORGANISM: Human
 US-09-817-181-4

Query Match 22.7%; Score 587.5; DB 10;
Best Local Similarity 41.6%; Pred. No. 4.8e-34;
Matches 124; Conservative 55; Mismatches 114; Indels 5;

Qy	18	QTPLRDHYLLGKKGOGGFTYLT	TEKST	SANYACKSIPRKKLYCREDYEDVWREIQI	77
Db	12	QAEIIRDIYDFROVLGTGAFSEVILAEDKRTQKLVAKICIAKEALSGEK--SMENEIAV	69		
Qy	78	MHILSHHPNVRUKGYEDSVFVHIWMEVCEGELFDRIVSGKHSFERAVKLITLIV	137		
Db	70	LHKI-KHPNI-VALDDIYESGHLIYLMQVSGELFDRIVEKGYFYTERDASRLIFQVDA	128		
Qy	138	VEACHSLGVMHRLKPENFLFDSPKDDAKLKAIDFGLSVFYKPGQYLVDWGSPYVAPE	197		
Db	129	VKYLHDLGIVHRLDKPENLIYXSLDEDSKIMTISDFGLSKMEDPGSVLSTACGTPGVVAPE	188		
Qy	198	VL-KCYGPBIDVWSAGVITLYILLSGVPPWAFETSGIERQILLOGKLDKPSDPWTISA	256		
Db	189	VLAQPYSKAVDCNSIGVAYILLGCGYPPFYDENDAKLFEQILKAYEYEDSPYWDIDIS	248		
Qy	257	AKDLIYMLERSPKKISIAHEALCHPWIVDEQAAPKPLDPVLSRLKQFSOMNKIKK	314		
Db	249	AKDF-IHLMKEKDPKFTCEQALQHPWIAJGDTAL-DKNIHQSVSEIQKKNFAKSKWKO	305		

RESULT 13
US-10-024-036B-2
; Sequence 2, Application US/10024036B

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; Publication No. US20030028004A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 68730 and 69112
; TITLE OF INVENTION: Molecules and
; FILE REFERENCE: MP12000-521Pr(M)
; CURRENT APPLICATION NUMBER: US/10/07
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/258222
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: RastSeq for Windows Version
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PPT
; ORGANISM: Homo sapiens
US-10-024-0368-2

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Query Match		21.4%;	Score 554;	DB 9;	Length 357;
Best Local Similarity		37.1%;	Pred. No. 1.le-31;		
Matches 117;	Conservative	66;	Mismatches 120;	Indels	12; Gaps
QY	32	LGOQFGTYLCTEKSTISANYACKSPKPKLLVCREDYEDVWREIQIMHHLSEHPVVRIK	91		
Db	29	LGTGAFSEWLAEAKTKGLFAVKCIPKKALAKGE--SSINEIAVLARKI-KHENIVALE	85		
QY	92	GTYEDSVFHVIMBVCSGGLFDRIIVSKGHFSEREAVKLITILGVVEACHSLGWHRDL	151		
Db	86	DYESPNNHYLMVNLWSGGELFDRIIVEKGFTYDEKDASTLIROVLDAVYLHRMGIVHRDL	145		
QY	152	KPENLFDSPPDKDALKATDFGLSVFKPQGVLVDVGVSPPYVAPEVL-KKCYPGEDVW	210		
Db	146	KPENLYYSQDEESKIMISDFGLSKMEGSDVMSTACGTFGVVAPEVLAQPYPSKAVDCW	205		
QY	211	SAGVILYILLGSVPFWAETESIGFIQILOGKLDTPKSDPWPTISEAAKDLITYKMLESRK	270		
Db	206	SIGVIAYTILCGYPFYDENDSLKFQILKAEFVEDSPYWDIDSDSAKDFIRNLMEXDPN	265		
QY	271	KRISAHEALCHPNIVDQAAPDKPLDPAVLSRL-KQFSOMNKIKMALVTAERKLEEEI	329		
Db	266	KRYTCQAARHPWTJAGTAL-NKNIIHESYSAQIRKNFKASQRQAFNAVTAVRHMRKHLH	324		

```

QY      330 GGLKELFKMIDTNS 344
      |
      :|:|:
Db      325 G-----SSLDSSNA 333

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RESULT 14
US-10-096

US-10-096-960-4
; Sequence 4, Application US/10096960
; Patent No. US20020132325A1

```

; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001158DIV
; CURRENT APPLICATION NUMBER: US/10/096,960
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/800,960
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-096-960-4

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Query Match	21.0%;	Score 543.5;	DB 12;	Length 556;
Best Local Similarity	37.0%;	Pred. No. 1e-30;		

Matches	120; Conservative	63; Mismatches	128; Indels	13; Gaps	5;				
QY	21	RLRDHYLLGKLGCGQGT	TTCLCTEKSTSAN	YACKSIPKRLKVC	REDYEDVYURETQIMHH 80				
Db	9	RFTDDYQLFEELGKGF	SVWRCKVKTST	QBYAAKIINTKKLS	AR-DHOKLEREARIC-R 66				
QY	81	LSEHPNVVRIKGT	YEDSVFVHIVME	CEGGELFDRIV	SKGHFSREAAVKLTITLGVVEA 140				
Db	67	LLKHPIVRLHDS	ISEEGFHYLV	FDLTGTGELF	EDIVAREYYSEADASHCIHQILES	VNH 126			
QY	141	CHSLGVMHRLDL	KNPFI	DFSPDKDAKL	KATDFGLSVFYK	PCQYL-YDVVGSPPYVAPEVL 199			
Db	127	IHQHDIVHRLDL	KNP	LLASCKGA	AAVKLADFLAIEV	QGGQAAWFGAGTGPLVSPVL 186			
QY	200	KK-CYGEIDVWS	AGVILYILL	SGVPPFWA	ETSGIFRQILQGL	KDFKSDPWRTISEAAK 258			
Db	187	RKDPYKGPV	DIWACGVILY	ILLVGP	PPFWEQDKHLYQ	IKAGAYDFSP	EMDVTVP	PEAK 246	
QY	259	DLAYKMLERS	PKKRISAE	ALCHPWIV	DEAQRAPDK	PLDPAVLSRL	KQFSQNNKTK	KMALR 318	
Db	247	NLNMUTII	IPAKRTI	ADQALKHP	WVCQ	RSIVASMMH	QRTEVCLR	FNARRK	LKGALIT 306
QY	319	VI-----	AERLSEET	IGGLK 333					
Db	307	TMLSVRN	FSAKSL	LNKKSG	GVK 330				

RESULT 15

US-09-935-464-3
; Sequence 3, Application US/09935464
; Publication No. US20030027153A1

```

: GENERAL INFORMATION:
:
: APPLICANT: Meyer, Joanne
: APPLICANT: Barrington-Martin, Rory
: APPLICANT: Parker, Alexander
: TITLE OF INVENTION: METHODS AND COM
: TITLE OF INVENTION: DISORDERS SUCH
: FILE REFERENCE: 3322/1H702 US1
: CURRENT APPLICATION NUMBER: US/09/9
: CURRENT FILING DATE: 2001-08-23
: PRIOR APPLICATION NUMBER: US 09/757
: PRIOR FILING DATE: 2001-01-09
: NUMBER OF SEQ ID NOS: 90
:

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1 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
2 ;
3 ; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA

; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 460
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-935-464-3

Query Match 20.9%; Score 543; DB 9; Length 460;
 Best Local Similarity 39.6%; Pred. No. 8.6e-31;
 Matches 116; Conservative 62; Mismatches 107; Indels 8; Gaps 6;

QY	18	QTPRLRDHYLLGKLGQGGTGYTLCTEKSTISANTYACKSIPKRLVCRDIEDVWREIQI	77
Db	15	QTTNIRKGTFIEMVLGSGAFSEVFLVKQLTGKLFALKCIKKSPAFROSSLEN---ETAV	71
QY	78	MHHLSEHPNVVRKIGTYEDSVFVHVMEVCEGGELFDRLIVSKGHFSEERAVKLITILGV	137
Db	72	LKKI-KHENIVTLEDIYESSTHYILVMQLVSGGELFDRLIERGVYTEKDASLVIQQVLSA	130
QY	138	VEACHSLGVMHRDLKPFDFSPKDDAKLKATDFGLSVFYKPGQYLYDVVCGSPYYVAPE	197
Db	131	VKYLHENGIVHRDLKPFENLLYTPENSKIMTDFGLSKMEONG-IMSTACGTPGYVAPE	189
QY	198	VL-KCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQKLDKFKSDPWPPTISEA	256
Db	190	VLAQPKYSKAVDCWSIGVITYILLGYPPEYETESKLFKEIKGYEYESFPFWDISES	249
QY	257	AKDLIYKMLERSPKRISNAHEALCHPWIVDEQAAPDKPLDPAV-LSRLKQFSQ	308
Db	250	AKDFICHLEKDPNRYTCEKALSHPWI-DGNTALHRDIYPSVSLQIQKNFAK	301

Search completed: March 26, 2003, 13:22:07
 Job time : 122 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 12:16:51 ; Search time 40 Seconds
(without alignments)
1189.663 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPIYQTP.....KNLNENIADAFVGDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2593	100.0	495	1 S46284	calcium-dependent
2	2458	94.8	501	2 G85097	hypothetical prote
3	2030	78.3	490	2 T08873	calcium-dependent
4	1944	75.0	508	1 A43713	calcium-dependent
5	1847.5	71.2	490	1 S71776	calcium-dependent
6	1752	67.6	492	1 T03271	calcium-dependent
7	1751	67.5	487	1 S71770	calcium-dependent
8	1745	67.3	554	1 T03263	calcium-dependent
9	1742	67.2	556	2 T06126	calcium-dependent
10	1731	66.8	544	2 D84550	calcium-dependent
11	1724	66.5	610	1 A49082	probable calmoduli
12	1709.5	65.9	573	2 T09940	calcium-dependent
13	1700.5	65.6	484	1 T05650	calcium-dependent
14	1672.5	64.5	639	1 T02784	calcium-dependent
15	1640.5	63.3	583	2 H84810	calcium-dependent
16	1630	62.9	451	2 S56717	probable calcium-d
17	1586	61.2	542	1 S56651	calcium-dependent
18	1484.5	57.3	540	1 T01989	calcium-dependent
19	1482	57.2	531	2 D85059	calcium-dependent
20	1480	57.1	531	1 S56652	probable calcium d
21	1480	57.1	531	1 T02993	calcium-dependent
22	1463.5	56.4	521	2 G96543	calcium-dependent
23	1462	56.4	529	1 S71774	calcium-dependent
24	1460.5	56.3	513	1 T02259	calcium-dependent
25	1460	56.3	534	1 JC1515	calcium-dependent
26	1458.5	56.2	538	2 T08874	calcium-dependent
27	1449	55.9	554	2 T05476	calcium-dependent
28	1437.5	55.4	465	1 T03024	calcium-dependent
29	1432.5	55.2	532	2 T14335	protein kinase, ca

30	1431	55.2	514	2 T10938	calcium-dependent
31	1381	53.3	545	2 H86322	calcium-dependent
32	1367.5	52.7	493	1 S46283	calcium-dependent
33	1363	52.6	541	2 F96776	hypothetical prote
34	1361	52.5	553	1 T02139	calcium-dependent
35	1356.5	52.3	520	2 F85059	calcium-dependent
36	1325.5	51.1	560	2 T46189	probable calcium d
37	1324.5	51.1	425	2 S17759	calcium-dependent
38	1313.5	50.7	533	1 S71778	protein kinase, ca
39	1287.5	49.7	520	2 C84774	calcium-dependent
40	1280.5	49.4	530	2 A84847	probable calcium-d
41	1238.5	47.8	582	2 E84721	probable Ca2+ depe
42	1229.5	47.4	575	2 C85059	probable calcium-d
43	1225.5	47.3	503	2 T51156	probable calcium d
44	1176.5	45.4	591	2 S54788	calcium-dependent
45	1056.5	40.7	571	2 T00835	calcium-stimulated
					calcium-dependent

ALIGNMENTS

RESULT 1

S46284

calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000

C:Accession: S46284

R:Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayashida, N.; Shi

Mol. Gen. Genet. 244, 331-340, 1994

A:Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by droug

A:Reference number: S46283; MUID:94359455; PMID:8078458

A:Accession: S46284

A:Molecule type: mRNA

A:Residues: 1-495 <URA>

A:Cross-references: EMBL:D21806; NID:gl235717; PIDN:BAA04830.1; PID:g604881

C:Genetics:

A:Gene: CbPK2

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-spec

F:24-284/Domain: protein kinase homology <KIN>

F:32-40/Region: protein kinase ATP-binding motif

F:327-359/Domain: calmodulin repeat homology <EFI>

F:363-395/Domain: calmodulin repeat homology <EF2>

F:399-431/Domain: calmodulin repeat homology <EF3>

F:433-465/Domain: calmodulin repeat homology <EF4>

F:55/Active site: Lys #status Predicted

Query Match

Best Local Similarity 100.0%; Score 2593; DB 1; Length 495;

Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METKPNRRPSNTVLPIYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPIKR 60

Db 1 METKPNRRPSNTVLPIYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPIKR 60

Qy 61 KLVCREDYEDVWRETIQIMHHLSEHPNVVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120

Db 61 KLVCREDYEDVWRETIQIMHHLSEHPNVVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120

Qy 121 HFSREAVKLIKTILGVVEACHSLGVHMDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180

Db 121 HFSREAVKLIKTILGVVEACHSLGVHMDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180

Qy 181 GQYLDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSSVPPFWAETESGIFROILO 240

Db 181 GQYLDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSSVPPFWAETESGIFROILO 240

Qy 241 GKLFKSDPWPPTISEAKNDLIYKMLERSPKKRISAHEALCHPWIIVDQAPDKPLDPAVL 300

Db 241 GKLFKSDPWPPTISEAKNDLIYKMLERSPKKRISAHEALCHPWIIVDQAPDKPLDPAVL 300

Qy 301 SRLKQFSCMNKKMKWALVIAERLSSEIIGLKELFKMDITDNGTITTFEELKAGLRVG 360

Db 301 SRLKQFSCMNKKMKWALVIAERLSSEIIGLKELFKMDITDNGTITTFEELKAGLRVG 360

Db 301 SRLKQFSQMNKIKKALVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVG 360
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYIT 420
Db 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYIT 420
QY 421 IDELQSACTEFLGCDTPLDDMKKEIDLNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 480
Db 421 IDELQSACTEFLGCDTPLDDMKKEIDLNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 480
QY 481 NIADAFVDGKSD 495
Db 481 NIADAFVDGKSD 495

RESULT 2
G85097
hypothetical protein At4g09570 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 23-Mar-2001
C:Accession: G85097
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85097
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <S>
A:Cross-references: NC_001268; NID:g7267652; PIDN:CAB78080.1; GSPDB:GN00140
C:Genetics:
A:Gene: At4g09570
A:Map position: 4
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: EF hand

Query Match 94.8%; Score 2458; DB 2; Length 501;
Best Local Similarity 94.8%; Pred. No. 1.6e-84;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRRPSNTVLPQTPLRDHYLLGKLGQGGTGYLCTEKTSTANYACKSTIPKRLV 63
Db 3 KPNRRPSNVLPETPLRDHYLLGKLGQGGTGYLCTEKTSTANYACKSTIPKRLV 62
QY 64 CREDYEDVWREIQIMHLSHPNVVRIGTYEDSVFVHVMVECGEGELFDRIYVSKGHES 123
Db 63 CREDYEDVWREIQIMHLSHPNVVRIGTYEDSVFVHVMVECGEGELFDRIYVSKGCF 122
QY 124 EREAVLIKILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQY 183
Db 123 EREAAKLIKILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQY 182
QY 184 LYDVVSGPYVAVPLKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243
Db 183 LYDVVSGPYVAVPLKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 242
QY 244 DFKSDPPTTISEAKOLIIYKMLDRSPKKRISAHEALCHPWIVDQAAAPDKPLDPVLSRL 303
Db 243 DFKSDPPTTISEAKOLIIYKMLDRSPKKRISAHEALCHPWIVDQAAAPDKPLDPVLSRL 302
QY 304 KQFSQMNKIKKALVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSEL 363
Db 303 KQFSQMNKIKKALVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSEL 362
QY 364 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDE 423
Db 363 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDE 422
QY 424 LQSACTEFLGCDTPLDDMKKEIDLNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 483
Db 423 LQSACTEFLGCDTPLDDMKKEIDLNDGKIDFSEFTAMMRKGDGVRSTMMKNLNF 482
QY 484 DAFGVDG----EKSD 495

Db 483 EAFGVEDTSTAKSD 498
:||||: ||||
:||||: EAFGVEDTSTAKSD 498

RESULT 3
T08873
calcium-dependent protein kinase (EC 2.7.1.1-) beta - soybean
C:Species: Glycine max (soybean)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T08873
R:Lee, J.Y.; Yoo, B.C.; Harmon, A.C.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z16505
A:Accession: T08873
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-490 <LEE>
A:Cross-references: EMBL:U69173; NID:g2501763; PID:g2501764
C:Genetics:
A:Gene: CDPK beta
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-speci
F:20-282/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:324-356/Domain: calmodulin repeat homology <EFH>
F:53/Active site: Lys #status predicted

Query Match 78.3%; Score 2030; DB 2; Length 490;
Best Local Similarity 81.1%; Pred. No. 1e-68;
Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;

QY 14 VLPYQTPRLRDHYLLGKLGQGGTGYLCTEKTSTANYACKSTIPKRLVCREDEYDVR 73
Db 12 VLPYQTPARLDHYLLGKLGQGGTGYLCTHKTGYLCKYACKSTIPKRLVCREDEYDVR 71
QY 74 EIQLMHLSHPNVVRIGTYEDSVFVHVMVECGEGELFDRIYVSKGHESEREAVLIK 133
Db 72 EIQLMHLSHPNVVRIGTYEDSVFVHVMVECGEGELFDRIYVSKGHESEREAVLIK 131
QY 134 ILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYIDYVVGSPY 193
Db 132 IVGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVILQARQAFHDVVGSPY 191
QY 194 VAPVLKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFSDPPTI 253
Db 192 VAPVLKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFSDPPTI 251
QY 254 SEAAKDLIIYKMLDRSPKKRISAHEALCHPWIVDQAAAPDKPLDPVLSRLKQFSQMNKIK 313
Db 252 SENAKELVKQMLDRDPKKRISAHEALCHPWIVDQAAAPDKPLDPVLSRLKQFSQMNKIK 310
QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSELMESEIKSLMD 373
Db 311 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSELMESEIKSLMD 370
QY 374 AADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDELOQSACTEFL 433
Db 371 AADIDNSGTIDYGEFLAATLHMKNKEREILVAAFSDFDKGSGYITIDELOQSACTEFL 430
QY 434 CDTPLDDMKKEIDLNDGKIDFSEFTAMMRKGDGVRSTMMKNLNFNIADAFV 488
Db 431 GDVHLDMEIKEDIDNDGIDYAEFAAMKKGDPNMGSRSTMMKNLNFNIADAFV 486

RESULT 4
A43713
calcium-dependent protein kinase (EC 2.7.1.1-) - soybean
C:Species: Glycine max (soybean)
C:Date: 03-Mar-1993 #sequence_revision 14-Jul-1994 #text_change 11-Jun-1999
C:Accession: A43713
R:Harper, J.F.; Sussman, M.R.; Schaller, G.E.; Putnam-Evans, C.; Charbonneau, H.; Ha
Science 252, 951-954, 1991
A:Title: A calcium-dependent protein kinase with a regulatory domain similar to calmo

A:Reference number: A43713; MUID:91240279; PMID:1852075

A:Accession: A43713

A:Molecule type: mRNA

A:Residues: 1-508 <HAR>

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin

F:32-292/Domain: protein kinase homology <KIN>

F:40-48/Region: protein kinase ATP-binding motif

F:335-367/Domain: calmodulin repeat homology <EF1>

F:371-403/Domain: calmodulin repeat homology <EF2>

F:407-439/Domain: calmodulin repeat homology <EF3>

F:441-473/Domain: calmodulin repeat homology <EF4>

F:63/Active site: Lys #status predicted

Query Match 75.0%; Score 1944; DB 1; Length 508;

Best Local Similarity 77.7%; Pred. No. 1.6e-65;

Matches 370; Conservative 51; Mismatches 51; Indels 4; Gaps 3;

QY 14 VLPYOTPLRDHYLLGKLGQOGFTTYLCTEKSANTYACKSIPKRLKVCREDYEDVWR 73

Db 22 VLPQRTQNIREVYEGKLGQOGFTTCTTRASGKGFACKSIPKRLKCKEDYEDVWR 81

QY 74 ETQIMHLLSEHPNVRIKGTEDSVFVHVMVEGEGELFDRIYKSGHSEAEVAKLIKT 133

Db 82 ETQIMHLLSEHANVRIETGSDSTAVHLVLMELCEGELFDRIYKSGHSEAEVAKLIKT 141

QY 134 ILGVVEACHSLGVMDHDKPENFLDSPKDDAKLKDTPGLSVFYKPGQYLDVVGSPYY 193

Db 142 IVEVVEACHSLGVMDHDKPENFLDTPIDEDAKLKDTPGLSVFYKPGSFCDVVGSPYY 201

QY 194 VAPEVLKCYGPEIDVWSAGVLYILLSGVPPFWAETSGIFRQILQKLGKDFSDPWPPT 253

Db 202 VAPEVLKCYGPEIDVWSAGVLYILLSGVPPFWAETSGIFRQILQKLGKDFSDPWPPT 261

QY 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPDPVLSRLKQFSOMNKT 313

Db 262 SDSAKDLIRKMLDQPKRLTAHEVLRHPWIVDDNAPDKPLDSAVLSRLKQFSAMNKLK 321

QY 314 KVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVGSSELSKSLMD 373

Db 322 KVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRVGSSELSKSLMD 381

QY 374 RADIDNSTIDYGEFLAATLHMKMEREEILVAASDFDKDGSYITIDELOSACETERGL 433

Db 382 RADIDNSTIDYGEFLAATLHMKMEREEILVAASDFDKDGSYITIDELOSACETERGL 441

QY 434 CDTPLDDMIKEIDLNDGKIDFSEPTAMMRKGD-GVGRSRMTMKNLNFIADAFGV 488

Db 442 DDHIEDDMKEIDLNDGKIDFSEPTAMMRKGD-GVGRSRMTMKNLNFIADAFGV 494

RESULT 5

S71776

calcium-dependent protein kinase (EC 2.7.1.1) 9 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Jun-1999

C:Accession: S71776; S71775; S71902; S71196

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.

Plant Mol. Biol. 30, 1259-1275, 1996

A:Title: Expression of three members of the calcium-dependent protein kinase gene family

A:Reference number: S71774; MUID:96311013; PMID:8704134

A:Accession: S71776

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-490 <HON>

A:Cross-references: EMBL:U20626

A:Accession: S71775

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-490 <HOF>

A:Cross-references: EMBL:U20388

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.

submitted to the EMBL Data Library, February 1995

A:Description: Expression of the calcium-dependent protein kinase gene family in Ara

A:Reference number: S71197

A:Accession: S71902

A:Molecule type: DNA

A:Residues: 1-164, 'S', '166-239, 'E', '241-300, 'KF', '303-350, 'S', '352-490 <HOW>

A:Cross-references: EMBL:U20626; NID:g836945; PIDN:AAA67657.1; PID:g836946

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua

submitted to the EMBL Data Library, January 1995

A:Description: Expression of the calcium dependent protein kinase gene family in Ara

A:Reference number: S71196

A:Accession: S71196

A:Molecule type: mRNA

A:Residues: 1-164, 'S', '166-239, 'E', '241-300, 'KF', '303-350, 'S', '352-490 <HOA>

A:Cross-references: EMBL:U20388; NID:g836937; PIDN:AAA67653.1; PID:g836938

C:Genetics:

A:Gene: CDPK9

A:Introns: 177/1; 225/1; 276/1; 370/3; 445/3

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-spec.

F:20-280/Domain: protein kinase homology <KIN>

F:28-36/Region: protein kinase ATP-binding motif

F:323-355/Domain: calmodulin repeat homology <EF1>

F:359-391/Domain: calmodulin repeat homology <EF2>

F:395-427/Domain: calmodulin repeat homology <EF3>

F:429-461/Domain: calmodulin repeat homology <EF4>

F:51/Active site: Lys #status predicted

Query Match 71.2%; Score 1847.5; DB 1; Length 490;

Best Local Similarity 73.5%; Pred. No. 5.6e-62;

Matches 355; Conservative 52; Mismatches 69; Indels 7; Gaps 2;

QY 1 METKPNRRPSTVLPYOTPLRDHYLLGKLGQOGFTTYLCTEKSANTYACKSIPK 60

Db 1 MANKPRTR----WLPYKTKNVEDNIFLGVLGQOGFTTFLCTKQTKLACKSIPK 56

QY 61 KLVCREDEYDVMREIQIMHLLSEHPNVRIKGTEDSVFVHVMVEGEGELFDRIYKSG 120

Db 57 KLLCQEDYDDVLRQIIMHLLSEHPNVRIKGTEDSVFVHVMVEGEGELFDRIYKSG 116

QY 121 HFSREAVKLIKTILGVVEACHSLGVMDHDKPENFLDSPKDDAKLKDTPGLSVFYK 180

Db 117 HYSEREAALIKTIYGVVEACHSLGVMDHDKPENFLDSPKDDAKLKDTPGLSVFYK 176

QY 181 GOYLDVVGSPYYVAPEVLKCYGPEIDVWSAGVLYILLSGVPPFWAETSGIFRQILQ 240

Db 177 GEAFSELVGSAYVAPEVLKHYGPECVWSAGVLYILLCGFPFWAETSGIFRQILQ 236

QY 241 GKLDPKSDPWPPTISAADLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPDPVLS 300

Db 237 GKLDPEINPWPSPISSEAKDLIKKMLSPKRLTAHQVLCHPWIVDDKVPDKPDCAV 296

QY 301 SRLKQFSOMNKTKKVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRV 360

Db 297 SRLKNGSAMNKKVALVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLRV 356

QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMKMEREEILVAASDFDKDGSYIT 420

Db 357 SELMESEIQELLRAADVDESGTIDYGEFLAATLHMKMEREEILVAASDFDKDGSYIT 416

QY 421 IDELOSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEPTAMMRKGDGVGRS---RTMK 477

Db 417 IEELQQAQWKEFGINDSLMDIKIDQDNDQIDYGEFVAMMRKNGTGGGIGRRTMNS 476

QY 478 LNF 480

Db 477 LNF 479

RESULT 6

T03271

calcium-dependent protein kinase (EC 2.7.1.1) 1 - maize

C:Species: Zea mays (maize)

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
C;Accession: T03271
R;Berberich, T.; Kusano, T.
Mol. Gen. Genet. 254, 275-283, 1996
A;Title: Cycloheximide induces a subset of low temperature-inducible genes
A;Reference number: Z14873
A;Accession: T03271
A;Status: translated from GE/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-492 <BER>
A;Cross-references: EMBL:D84408; PIDN:BAAL2338.1
A;Experimental source: strain honey bantum
A;Note: low temperature-inducible
C;Genetics:
A;Gene: CDPk1

C: Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
 C; Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F: 25-285/Domain: protein kinase homology <KIN>
 F: 33-41/Region: protein kinase ATP-binding motif
 F: 328-360/Domain: calmodulin repeat homology <EF1>
 F: 364-396/Domain: calmodulin repeat homology <EF2>
 F: 400-432/Domain: calmodulin repeat homology <EF3>
 F: 434-466/Domain: calmodulin repeat homology <EF4>
 F: 56/Active site: Lys #status predicted

Query Match 67.6%; Score 1752; DB 1; Length 492;
Best Local Similarity 70.6%; Pred. No. 1.9e-58;
Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;

QY	13	TVLPYOTPLRLDHYLHGKLLGQOGQFTTYLCTEKTSANYACKSPKRRKLVCREDYEDYW	72
Db	14	SVLGHTTPNLRLDHYALGRLGQOGFTTYLCTELATIDYAKSISKRLLITKEDVDVR	73
QY	73	REIQIMHLSHEPNVYRIKGTVEDSVFHVMEVCEGSEFLDRIYVSKGHFSEREAVKLK	132
Db	74	REIQIMHLSGHKNVVAIKGAYEDQYVHVLMELCAGGELFDRIQGHYSEKKAALTR	133
QY	133	TIILGVVEACHSLGVMRDLKPENFLIPDSKPDAAKLKATDGLSVFYKPGQYLYDVVWGSPY	192
Db	134	TIIVGVVEACHSLGVMRDLKPENFLIANRDDLSIKAIIDGLSVFFKPGQVTDVVWGSPY	193
QY	193	YVAPEVLKCYGPEIDWVSAGVITYILLSGVPFFWAAETESGIFRQILQGLDKDFKSDPWP	252
Db	194	YVAPEVLLKSYGPAADWTVAGVITYILLSGVPFFWAEIOQGIFDVAVLKAIDFSDPWPV	253
QY	253	ISBAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAPDKPLDPAVLSRLXQFSOMNKI	312
Db	254	ISDSAKDLIRMLNPRPAERLTAHEVLCHPWIRHGCVAPDRPLDPAVLSRIKQFSAMNKL	313
QY	313	KKMALVIAERLSEERIGGLKFLFKMIDTNSGTITFELKAGLRKVGSELMSEIKSLM	372
Db	314	KKMALVIAESJSEEBIAGLKEMQFMDTNSGAIITYDELKGLRYKYSTLKDITRIDL	373
QY	373	DAADIDNSGTIDYGEFLAATLHNMKMEREEILVAASFDPDKDGSYITIDEQSSACTEFG	432
Db	374	DAADIDNSGTIDYIEFTIATLHLNLEREEHLVAAFSYFDKDGSGYITVDELQLACKEH	433
QY	433	LCDTPLDDMIKEILDIDNCKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIAD	484
Db	434	MPDAFVDVINEADQNDGRIDYGEFVAMTTKGNMGVGR-RTWRNSLNTSMRD	485

RESULT 7
S71770
calcium-dependent protein kinase (EC 2.7.1.1) - mung bean
C:Species: Vigna radiata (mung bean)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-Jun-1999
C:Accession: S71770
R:Botella, J.R.; Arteca, J.M.; Somodevilla, M.; Arteca, R.N.
Plant Mol. Biol. 30, 1129-1137, 1996
A>Title: Calcium-dependent protein kinase gene expression in response to physical and chemical stresses in mung bean
A:Reference number: S71770; MOID:96311003; PMID:8704124
A:Accession: S71770

A; Molecule type: mRNA
A; Residues: 1-487 <BOT>
A; Cross-references: EMBL:U08140; NID:g967124; PTDN:AAC49405.1; PID:g967125
A; Experimental source: strain Rwlcz, cv. Berken, clone pYr-CDPK-1
C; Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
C; Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F; 22-282/Domain: protein kinase homology <KIN>
F; 30-38/Region: protein kinase ATP-binding motif
F; 325-357/Domain: calmodulin repeat homology <EF2>
F; 361-393/Domain: calmodulin repeat homology <EF3>
F; 397-429/Domain: calmodulin repeat homology <EF4>
F; 431-463/Domain: calmodulin repeat homology <EF5>
F; 53/Active site: Lys #status predicted

Query Match 67.5%; Score 1751; DB 1; Length 487;

Best Local Similarity 69.1%; Pred. No. 2e-58;
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;

Qy	14	VLPQTPRLRDHYLLGKLGQGGFTTYLCTEKSTANYACKSIPKRKLVCREDYEDVWR	73
Db	12	VLGHKTENIRDLTGLRKLGGQGGFTTYLCTENSTNEYACKSISKRKLSEKEDVEDRR	71
Qy	74	EIQMHLSBHPNVRUKGYEDSVFVHIIWVECEGELFDRIVSKGHSERSEPAVLKLT	133
Db	72	EIQMHLAGKNVITLKGAYEDPLVHIIWVEJCSGELFDRIIQGHYTERKAELTKI	131
Qy	134	ILGVVEACHSLGMVHRDLKPENFLDPSKDDAKLKATDFGLSFYFKPGQYLDVVGSPYY	193
Db	132	IVGVVEACHSIGVMHRDLKPENFLLVNKDDDFSLKIDFGLSFYFKPGQITFDVVGSPYY	191
Qy	194	VAPVLKCKCPEDLDVWSAGVILYLLSGVPPFAETESIFRQILOGKLDPKSDDWPTI	253
Db	192	VAPVLKUHGPADVMTAGVILYLLSGVPPFAETQOIGIDAVILKGRHIDFSDDWPTI	251
Qy	254	SEAKDLIYKMLSPSKRISAEALCHPWIVDEQAPDKPLDPAYLSRLKQFSQMNKIK	313
Db	252	SDSGKDIRKMLCSQPSERUTAHQVLCPWICENGVAPORAIDPAVLSRLKQFSAMNKLK	311
Qy	314	KMALRVABRLSEETIGLKEPKMIDTDSNGITTEELKAGLKRVGSELMSEITSKMD	373
Db	312	KMALRVATLSSEETIAGLRNFQAMDTDSNGAITTDELKAGLURRYGSTLKQVEIRDLME	371
Qy	374	AADIDNSGTDYGEFLAATLHMNMEREELLVAASFDFDKDGSYITIDELOSACFEGL	433
Db	372	AADVKSGTIDYGEFLAATVHLNKLREEHILAAFYFDFKDGSGYITVELQOACAEHNM	431
Qy	434	CDTFLDMIKELDNDGKTDIDSEFTAMMRKGD-GVGRSRTMKNLNFNIADA	485
Db	432	TDALFIDIREVQDNDGRIDYGEFAAMQKGNAGIGR-RTMNSLNLMSRDA	483

RESULT 8
T03263

103203
calcium-dependent protein kinase (EC 2.7.1.-) 7 - maize

C; Species: Zea mays (maize)

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T03263

R; Saijo, Y.; Hata, S.; Sheen, J.; Izui, K.

Biochim. Biophys. Acta 1350, 109-114, 1997

A:Title: CDNA cloning and prokaryotic expression of the human CDNA 13307, 13314, 13315, 13316, 13317, 13318, 13319, 13320, 13321, 13322, 13323, 13324, 13325, 13326, 13327, 13328, 13329, 13330, 13331, 13332, 13333, 13334, 13335, 13336, 13337, 13338, 13339, 13340, 13341, 13342, 13343, 13344, 13345, 13346, 13347, 13348, 13349, 13350, 13351, 13352, 13353, 13354, 13355, 13356, 13357, 13358, 13359, 13360, 13361, 13362, 13363, 13364, 13365, 13366, 13367, 13368, 13369, 13370, 13371, 13372, 13373, 13374, 13375, 13376, 13377, 13378, 13379, 13380, 13381, 13382, 13383, 13384, 13385, 13386, 13387, 13388, 13389, 13390, 13391, 13392, 13393, 13394, 13395, 13396, 13397, 13398, 13399, 13400, 13401, 13402, 13403, 13404, 13405, 13406, 13407, 13408, 13409, 13410, 13411, 13412, 13413, 13414, 13415, 13416, 13417, 13418, 13419, 13420, 13421, 13422, 13423, 13424, 13425, 13426, 13427, 13428, 13429, 13430, 13431, 13432, 13433, 13434, 13435, 13436, 13437, 13438, 13439, 13440, 13441, 13442, 13443, 13444, 13445, 13446, 13447, 13448, 13449, 13450, 13451, 13452, 13453, 13454, 13455, 13456, 13457, 13458, 13459, 13460, 13461, 13462, 13463, 13464, 13465, 13466, 13467, 13468, 13469, 13470, 13471, 13472, 13473, 13474, 13475, 13476, 13477, 13478, 13479, 13480, 13481, 13482, 13483, 13484, 13485, 13486, 13487, 13488, 13489, 13490, 13491, 13492, 13493, 13494, 13495, 13496, 13497, 13498, 13499, 13500, 13501, 13502, 13503, 13504, 13505, 13506, 13507, 13508, 13509, 13510, 13511, 13512, 13513, 13514, 13515, 13516, 13517, 13518, 13519, 13520, 13521, 13522, 13523, 13524, 13525, 13526, 13527, 13528, 13529, 13530, 13531, 13532, 13533, 13534, 13535, 13536, 13537, 13538, 13539, 13540, 13541, 13542, 13543, 13544, 13545, 13546, 13547, 13548, 13549, 13550, 13551, 13552, 13553, 13554, 13555, 13556, 13557, 13558, 13559, 13560, 13561, 13562, 13563, 13564, 13565, 13566, 13567, 13568, 13569, 13570, 13571, 13572, 13573, 13574, 13575, 13576, 13577, 13578, 13579, 13580, 13581, 13582, 13583, 13584, 13585, 13586, 13587, 13588, 13589, 13590, 13591, 13592, 13593, 13594, 13595, 13596, 13597, 13598, 13599, 13600, 13601, 13602, 13603, 13604, 13605, 13606, 13607, 13608, 13609, 13610, 13611, 13612, 13613, 13614, 13615, 13616, 13617, 13618, 13619, 13620, 13621, 13622, 13623, 13624, 13625, 13626, 13627, 13628, 13629, 13630, 13631, 13632, 13633, 13634, 13635, 13636, 13637, 13638, 13639, 13640, 13641, 13642, 13643, 13644, 13645, 13646, 13647, 13648, 13649, 13650, 13651, 13652, 13653, 13654, 13655, 13656, 13657, 13658, 13659, 13660, 13661, 13662, 13663, 13664, 13665, 13666, 13667, 13668, 13669, 13670, 13671, 13672, 13673, 13674, 13675, 13676, 13677, 13678, 13679, 13680, 13681, 13682, 13683, 13684, 13685, 13686, 13687, 13688, 13689, 13690, 13691, 13692, 13693, 13694, 13695, 13696, 13697, 13698, 13699, 13700, 13701, 13702, 13703, 13704, 13705, 13706, 13707, 13708, 13709, 13710, 13711, 13712, 13713, 13714, 13715, 13716, 13717, 13718, 13719, 13720, 13721, 13722, 13723, 13724, 13725, 13726, 13727, 13728, 13729, 13730, 13731, 13732, 13733, 13734, 13735, 13736, 13737, 13738, 13739, 13740, 13741, 13742, 13743, 13744, 13745, 13746, 13747, 13748, 13749, 13750, 13751, 13752, 13753, 13754, 13755, 13756, 13757, 13758, 13759, 13760, 13761, 13762, 13763, 13764, 13765, 13766, 13767, 13768, 13769, 13770, 13771, 13772, 13773, 13774, 13775, 13776, 13777, 13778, 13779, 13780, 13781, 13782, 13783, 13784, 13785, 13786, 13787, 13788, 13789, 13790, 13791, 13792, 13793, 13794, 13795, 13796, 13797, 13798, 13799, 13800, 13801, 13802, 13803, 13804, 13805, 13806, 13807, 13808, 13809, 13810, 13811, 13812, 13813, 13814, 13815, 13816, 13817, 13818, 13819, 13820, 13821, 13822, 13823, 13824, 13825, 13826, 13827, 13828, 13829, 13830, 13831, 13832, 13833, 13834, 13835, 13836, 13837, 13838, 13839, 13840, 13841, 13842, 13843, 13844, 13845, 13846, 13847, 13848, 13849, 13850, 13851, 13852, 13853, 13854, 13855, 13856, 13857, 13858, 13859, 13860, 13861, 13862, 13863, 13864, 13865, 13866, 13867, 13868, 13869, 13870, 13871, 13872, 13873, 13874, 13875, 13876, 13877, 13878, 13879, 13880, 13881, 13882, 13883, 13884, 13885, 13886, 13887, 13888, 13889, 13890, 13891, 13892, 13893, 13894, 13

A: Reference number: Z14815; MUID: 97201047.

A:Accession: T03263
n/Referencec number: Z14015, M01D: 97201047,

A: Status: translated from GR/EMBL/DDBT

A: Molecule type: mRNA

A:Residues: 1-554 ✓SAT✓

A,RESIDUES: I-334 <SAI>
A:Cross-references: EMPRI.D87043. NTD..21504051. DTOW 03310000 1501020

A; Cross-References: EMBL:D87042; NID:G1504051; PIDN:BAA132

Cell source: strain inbred line H84, clone CDPK7

C; superfamily: calcium-dependent protein kinase; calmodulin

C; keywords: ATP; calcium binding; EF hand; phosphotransfer

F;89-349/Domain: protein kinase homology <KIN>

F:97-105/Region: protein kinase ATP-binding motif

F:392-424/Domain: calmodulin repeat homology <EF1>

F;428-460/Domain: calmodulin repeat homology <EF2>

QY 6 N PRRPSNTVLPYQTPRLRDHYLLGKKLGQGFQGTYYLCTEKSTSANYACKSIPKRKLVC 65

D6 125 EDVEDVRREIQIMHHLAGHKNIVTIKGAYEDPLYVHIVMELCAGGELFDRIIHRGHYSER 184

QY 6 N PRRPSNTVLPYQTPRLRDHYLLGKKLGQGFQGTYYLCTEKSTSANYACKSIPKRKLVC 65

Db 185 KAAELTKIIVGVVEACHSLGVHWRDLKPENFLLVKNDDDFSLKATDFGLSVFFKFGQIFK 244
 QY 186 DVVGSPIYVAPVLLKCKGPEIDVWSAGVILYILSGVPPFWAETESGIFRQIOGLKDF 245
 Db 245 DVVGSPIYVAPVLLKCKGPEIDVWSAGVILYILSGVPPFWAETESGIFRQIOGLKDF 304
 QY 246 KSDPMTTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQOAPDPLDPAVLSRLKQ 305
 Db 305 DTDPPVLSDSAKDLIRKMLCSPSERLTAHEVLRHPWICENGVPDRALDPVLSRLKQ 364
 QY 306 FQOMNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLRKRGSELM 365
 Db 365 FQOMNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLRKRGSELM 424
 QY 366 SEIKSLMDAADTNSGTTIDYGFELATLHMKNKEREELIVAFSDFDKDGSYIIDELO 425
 Db 425 TEIRDLMEAADVNSGTTIDYSEFIATHLNKLEREELVSAFYDFDKDGSYIIDELO 484
 QY 426 SACTEFGLCDTFLDMDIKEDIDNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIAD 484
 Db 485 QSCIEHGMDVLEDLIKEDVDQDNGRIDYEEFVAMQKGNAGVR-RTMKNLSLMSMRD 543
 RESULT 11
 A49082
 calcium-dependent protein kinase (EC 2.7.1.1) AK1 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 14-May-1998 #sequence_revision 14-May-1999 #text_change 11-Jun-1999
 C:Accession: A49082
 R:Harper, J.F.; Binder, B.M.; Sussman, M.R.
 Biochemistry 32, 3282-3290, 1993
 A:Title: Calcium and lipid regulation of an Arabidopsis protein kinase expressed in Esch
 A:Reference number: A49082; MUID:93213795; PMID:7916621
 A:Contents: ecotype Columbia
 A:Accession: A49082
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <HAR>
 A:Cross-references: GB:L4771; NID:q289189; PIDN:AAA32761.1; PID:q304105
 A:Note: sequence extracted from NCBI backbone (NCBIN:128903, NCBI:P:128904)
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
 C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F:148-408/Domain: protein kinase homology <KIN>
 F:156-164/Region: protein kinase ATP-binding motif
 F:451-483/Domain: calmodulin repeat homology <EF1>
 F:487-519/Domain: calmodulin repeat homology <EF2>
 F:523-555/Domain: calmodulin repeat homology <EF3>
 F:557-589/Domain: calmodulin repeat homology <EF4>
 F:179/Active site: Lys #status predicted

Query Match 66.5%; Score 1724; DB 1; Length 610;
 Best Local Similarity 65.5%; Pred. No. 2.5e-57;
 Matches 329; Conservative 62; Mismatches 91; Indels 20; Gaps 2;

QY 2 ETKP-----NPRP-----SNTVLPYQTPRDRDHYLLGKKGQGGFGTTY 41
 Db 106 ETKPESKDPAPKPKPKHMKRVSSAGLRTESVLQRTKNEFEYSGLRKLQGGFGTTF 165
 QY 42 LCTEKSTANVACKSIPRKLKVCREDYEDVWREIQTIMHLSHPNNVRIKGYEDSVFVH 101
 Db 166 LCVETKTEACKSIARKLKLTDEVEDVRREIQTIMHLAGHPNVIISIKGAYEDVAVH 225
 QY 102 IYMEVCEGELPDRIVSKGHFSEREAVKLITILGVVEACHSLGVHWRDLKPENLFDSP 161
 Db 226 IYMECCAGGELFDRILQIRGHYTERKAAELTRITGVVEACHSLGVHWRDLKPENLFSK 285
 QY 162 KDAKLKATDFGLSVFYKPGQVLYDWVGSPIYVAPVLLKCKGPEIDVWSAGVILYILS 221
 Db 286 HEDSLKTIIDFGLSMFEKPDVFTDVGSPYVAPVLLKCKGPEIDVWSAGVILYILS 345
 QY 222 GYPFWAETESGIFRQIOGLKDFKSDPWTPTISAAKDLIYKMLERSPKKRISAHEALCH 281
 Db 346 GYPFWAETESGIFRQIOGLKDFKSDPWTPTISAAKDLIYKMLERSPKKRISAHEALCH 405

QY 282 PWIVDQOAPDPLDPVLSRLKQFSQMNKIKKMLARVIAERLSEEEIGGLKELFKMIDT 341
 Db 406 PWVQVDGVPADPLDSAVLSRLMKQFSAMNKKFMMALRVIAERLSEEEIAGLKMENMIDA 465
 QY 342 DNSGTTTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQOAPDPLDPVLSRLKQ 401
 Db 466 DKSQGITTEELKAGLRKRGSELMSEIKSLMDAADTNSGTTIDYGFELATLHMKNKERE 525
 QY 402 EILVAAFDFDKDGSYITIDELOQACTEFGLCDTFLDMDIKEDIDNDGKIDFSEFTAM 461
 Db 526 DHLFAFTYFDKDGSIYTPDELQACEEFGVEDVRIELMRDVPDQDNGRIDYNEFYAM 585
 QY 462 MRKGDGVRGSRRTMMKNLNFNTA 483
 Db 586 MQKSGITGTPVKMGLKSFSTIA 607
 RESULT 12
 T09940
 calcium-dependent protein kinase (EC 2.7.1.1) CDPK - pumpkin
 N:Alternate names: calcium-dependent calmodulin-independent protein kinase CDPK
 C:Species: Cucurbita pepo (pumpkin)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09940
 R:Ellard-Ivey, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.
 Plant Mol. Biol. 39, 199-208, 1999
 A:Title: Cloning, expression and N-terminal myristoylation of CcpPK1, a calcium-depen
 A:Reference number: 216898; MUID:99178773; PMID:10080688
 A:Accession: T09940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-573 <ELL>
 A:Cross-references: EMBL:U90262; NID:gl899174; PIDN:AAB49984.1; PID:gl899175
 A:Experimental source: etiolated hypocotyls
 C:Genetics: A:Gene: CPK1
 C:Function: A:Description: serine/threonine-specific protein kinase activated by direct binding c
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
 C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphot
 F:108-368/Domain: protein kinase homology <KIN>
 F:447-479/Domain: calmodulin repeat homology <EFH>

Query Match 65.9%; Score 1709.5; DB 2; Length 573;
 Best Local Similarity 64.8%; Pred. No. 8e-57;
 Matches 321; Conservative 78; Mismatches 79; Indels 17; Gaps 3;

QY 4 KPNRP-----RP-----SNTVLPYQTPRDRDHYLLGKKGQGGFGTTYLCTEKS 47
 Db 72 KPEPPMEPKVRPMKRVSGAGLRGGSVLQTKTGNFKYSLGKGLGQGGFGTTYMCVEKA 131
 QY 48 TSANYACKSIPRKLKVCREDYEDVWREIQTIMHLSHPNNVRIKGYEDSVFVHIVMEVC 107
 Db 132 TGKEYACKSIARKLKVNEDVEDVRREIQTIMHLSGHPNVIISIKGAYEDAVAVQVVMELC 191
 QY 108 EGGELEFDRIVSKGHFSEREAVKLITILGVVEACHSLGVHWRDLKPENLFDSPKDDAKL 167
 Db 192 AGGELFDRILQIRGHYTERKAAELTRITGVVEACHSLGVHWRDLKPENLFDVFSKEEELL 251
 QY 168 KATDFGLSVFYKPGQVLYDWVGSPIYVAPVLLKCKGPEIDVWSAGVILYILSGVPPFW 227
 Db 252 KTIIDFGLSMFEKPGKFNVDVGSPYVAPVLLKCKGPEIDVWSAGVILYILSGVPPFW 311
 QY 228 AETESGIFRQIOGLKDFKSDPWTPTISAAKDLIYKMLERSPKKRISAHEALCHPWIVD 287
 Db 312 AESERGIEEVLHGLDFFSDPWPSPISDAKDLVRLMLVRDPRKRLTAYELVCHPWVQVD 371
 QY 288 QAAPKPLDPVLSRLKQFSQMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTI 347
 Db 372 GVADPKPLDSAVLTLKQFSAMNKKFMMALRVIAERLSEEEIAGLKMFKMIDTNSGQI 431
 QY 348 TFEELKAGLRKRGSELMSEIKSLMDAADTNSGTTIDYGFELATLHMKNKEREELVAA 407

Db 432 TFEEELKAGLKKFGANLKESEIYDLMOQAADINNGTTIDYGEFVAATILHLNKEDEHLLAA 491
QY 408 FSDFDKDGSGYITIDELQSACTEFGCLDPLODMKEIDLNDGKIDPSEFTAMMRKGDG 467
Db 492 FSDFDKDGSGFIITHELDQACKEFGIEDLQEMEMREVNDNGSDIDYNEFVAMMKGV 551
QY 468 VGRSRTMKMLNFENI 482
Db 552 VNTGKKQLQS-SFSI 565
RESULT 13
T05650
N:calcium-dependent protein kinase (EC 2.7.1.1.) F20D10.350 - Arabidopsis tha
C:Alternate names: protein F20D10.350
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
C:Accession: T05650
R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15420
A:Accession: T05650
A:Molecule type: DNA
A:Residues: 1-484 <REV>
A:Cross-references: EMBL:AL035538
A:Experimental source: cultivar Columbia; BAC clone F20D10
C:Genetics:
A:Map position: 4
A:Insertions: 179/1; 227/1; 278/1; 316/3; 372/3; 447/3
A:Note: F20D10.350
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology
C:Keywords: Arp; calcium binding; EF hand; phosphotransferase; serine/threo
F; 22-282/Domain: protein kinase homology <XIN>
F; 30-38/Region: protein kinase Arp-binding motif
F; 325-357/Domain: calmodulin repeat homology <EF1>
F; 361-393/Domain: calmodulin repeat homology <EF2>
F; 397-429/Domain: calmodulin repeat homology <EF3>
F; 431-463/Domain: calmodulin repeat homology <EF4>
F; 53/Active site: Lys #status predicted

[illegible]

probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C:Accession: H84810

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84810

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-583 <STO>

A:Cross-references: GB:AE002093; NID:g3928078; PIDN:AAC79604.1; GSPDB:GN00139

C:Genetics:

A:Gene: Atg38910

A:Map position: 2

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin

C:Keywords: EF hand

Query Match 63.3%; Score 1640.5; DB 2; Length 583;
Best Local Similarity 66.9%; Pred. NO. 2.9e-54;
Matches 307; Conservative 67; Mismatches 84; Indels 1; Gaps 1;

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QY 12 NTVLPYQPRLDHYLLKGLGOGFGTTLCTEKSTSANACKSIPKRLVCREDYEDV 71
Db 120 DSVLGRKTENKDIYSVGRKLGOGFGTFLCVDRKTKFEACKTIARKKLTTPEDVEDV 179

QY 72 WREIQIMHHLSEHPNVVRKGTYESVFIYMEVCEGSELEFDRIVSKGHFSEBAVKLI 131
Db 180 RREIQIMHHLSEHPNVQIVGAYEDAVAVHVMIEICAGSELEFDRIIQRCHYTEKKAELA 239

QY 132 KTLGVVEACHSLGYMHRDLKPNFLDSPKDDAKLKATDFGLSVFYKPGQVLYDVGSP 191
Db 240 RIIVGVIEACHSLGYMHRDLKPNFLFVSGDDEAAKTIIDFGLSVFFKPGFTFTDVGSP 299

QY 192 YVVAPEVLKCYGPEIDVWSAGVILYILSGVPPFWAETESGIFRQILQGKLDKSDPWP 251
Db 300 YVVAPEVLKHYSHCEDVWSAGVILYILSGVPPFWDETEQGEVQLKGLDLDIFSEWP 359

QY 252 TISEAKDLIYKMLERSPKKRISAHEALCHPWIVDQAPKPLDPVLSRLKQFSQNMK 311
Db 360 SVSESAKDLVRMLTRDPKRMTHTEVLCHPWAVDGVVALDKPLDSAVLSRLQQFSAMNK 419

QY 312 IKKALRYIAEELSEEEIGGLKELFKMTDTONSGTITEELKAGLRVGSSELMSEIKSL 371
Db 420 LKKIAIKVIAEELSEEEIAGUKEMFKMTDTONSGHITLLELKKGLDRYGADLKDSEILGL 479

QY 372 MDAADINSGTIDYGEFTLAATLHMNMEREELVAAFSDFDKDQSGYITIDFLQSACTEF 431
Db 480 MDAADINSGTIDYGEFTAAVHLNLIKEDHLFTAFSYFDQDQSGYITRDELQQAACKQF 539

QY 432 GLCDTPLDMDIKEDLDNDGKIDFSEFTAMMKKGDGVR 470
Db 540 GLADVHLDLILREVDKONDGRIDYSEFYDDMM-QDTGFGK 577
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Search completed: March 26, 2003, 13:13:14
Job time : 43 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 11:57:52 ; Search time 22 Seconds

(without alignments)
933.217 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTP.....KNLNFNIADAFQVGEKSD 495

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1944	75.0	508	1	CDPK_SOYBN
2	1724	66.5	610	1	CDP1_ARATH
3	1586	61.2	542	1	CDP3_ORYSA
4	1482	57.2	533	1	CDP2_ORYSA
5	1460	56.3	513	1	CDP2_MAIZE
6	1460	56.3	534	1	CDP1_ORYSA
7	1432.5	55.2	532	1	CDPK_DAUCA
8	854	32.9	602	1	CRK_DAUCA
9	591	22.8	499	1	KCCD_HUMAN
10	589.5	22.7	374	1	KCC1_RAT
11	587.5	22.7	370	1	KCC1_HUMAN
12	578.5	22.3	473	1	KCC4_HUMAN
13	574.5	22.2	533	1	KCCD_RAT
14	574	22.1	469	1	KCC4_MOUSE
15	572	22.0	474	1	KCC4_RAT
16	571.5	22.0	542	1	KCCB_MOUSE
17	569.5	22.0	542	1	KCCB_RAT
18	567.5	21.9	478	1	KCCA_HUMAN
19	566.5	21.8	664	1	KCCB_HUMAN
20	563.5	21.7	478	1	KCCA_RAT
21	549.5	21.2	478	1	KCCA_MOUSE
22	544.5	21.0	529	1	KCCG_MOUSE
23	543.5	21.0	472	1	KCCG_HUMAN
24	539	20.8	527	1	KCCG_RAT
25	534.5	20.6	424	1	KPSH_HUMAN
26	533.5	20.6	386	1	KPBH_HUMAN
27	532.5	20.5	386	1	KPBH_RABIT
28	526	20.3	387	1	KPBG_RAT
29	524.5	20.2	387	1	KPBG_MOUSE
30	514.5	19.8	295	1	KMLC_DICDI
31	509	19.6	1431	1	DAPK_HUMAN
32	505	19.5	433	1	DKK1_RAT
33	505	19.5	740	1	DKK1_HUMAN

34	505	19.5	756	1	DKK1_MOUSE
35	499	19.2	335	1	KCC1_SCHPO
36	489.5	18.9	752	1	K6AA_CHICK
37	486	18.7	735	1	K6AL_RAT
38	484.5	18.7	512	1	K110_ARATH
39	482.5	18.6	733	1	K6A2_HUMAN
40	481	18.5	724	1	K6AL_MOUSE
41	480	18.5	735	1	K6AL_HUMAN
42	479	18.5	546	1	CHK2_MOUSE
43	477	18.4	733	1	K6AA_XENLA
44	476.5	18.4	733	1	K6A2_MOUSE
45	476	18.4	543	1	CHK2_HUMAN

ALIGNMENTS

RESULT 1
CDPK_SOYBN STANDARD; PRT; 508 AA.
AC P28583;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase SK5 (EC 2.7.1.1-) (CDPK).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams;
RX MEDLINE=91240279; PubMed=1852075;
RA Harper J.F., Sussman M.R., Schaller G.E., Putnam-Evans C.,
RA Charbonneau H., Harmon A.C.;
RT "A calcium-dependent protein kinase with a regulatory domain similar
to calmodulin."
RL Science 252:951-954(1991).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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EMBL; M64987; AAB00806.1;
DR PIR; A43713; A43713.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S-TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Calcium-binding; Phosphorylation.
 FT DOMAIN 34 292 PROTEIN KINASE.
 FT NP_BIND 40 48 ATP (BY SIMILARITY).
 FT BINDING 63 63 ATP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT CA_BIND 348 359 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 384 395 EF-HAND 2 (POTENTIAL).
 FT CA_BIND 420 431 EF-HAND 3 (POTENTIAL).
 FT CA_BIND 454 465 EF-HAND 4 (POTENTIAL).
 SQ SEQUENCE 508 AA; 57169 MW; AFDCE51224192E4 CRC64;

Query Match 75.0%; Score 1944; DB 1; Length 508;
 Best Local Similarity 77.7%; Pred. No. 2e-90;
 Matches 370; Conservative 51; Mismatches 51; Indels 4; Gaps 3;

QY 14 VLPQTPRLRDHYLLGKLGQGGFTYLTCTKSTSNANYACKSIPKRLKVCREDYEDVWR 73
 DB 22 VLPQTPQIRVEYVGRKLGQGGFTTCTRRASGGKFAKSPKRLKCKEDYEDVWR 81
 QY 74 EIQIMHLSHPNNVRIKGYEDSVFVHYMEYCEGELFDRIYKSGHFSERAVKLKT 133
 DB 82 EIQIMHLSHANVRIEGYEDSTAVHLVMEYCEGELFDRIYKSGHFSERAVKLKT 141
 QY 134 ILGVWACHSLGVMHRLKPFNLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVGSPYY 193
 DB 142 IVEVWEACHSLGVMHRLKPFNLFDSPKDDAKLKATDFGLSVFYKPGESFCDVGSPYY 201
 QY 194 VAPEVLKCKYGPEDVWSAGVILYLLSGVPPFWAETESIFRQILQGLKDFSDFWPTI 253
 DB 202 VAPEVLKCKYGPEDVWSAGVILYLLSGVPPFWAETESIFRQILQGLKDFSDFWPTI 261
 QY 254 SEAAKDLIYKMLRSPKRRISAHEALCHPWIVDEQAAPDKPLDPAYLSRLKQFSQNMKK 313
 DB 262 SDSAKDLIRKMLDQNEKTRLTAEVLRHPWIVDNTAPDKPLDSAVLSRLKQFSQNMKK 321
 QY 314 KMAIRVIAERLSEEBEGGLKELPKMIDTNSGTTITPEELKAGLKRVGSELMSEIKSLMD 373
 DB 322 KMAIRVIAERLSEEBEGGLKELPKMIDTNSGTTITPEELKAGLKRVGSELMSEIKSLMD 381
 QY 374 AADIDNSGTYDEFLAATLHMKMERETLVAASFDEKDGSGYITIDELQACATFGL 433
 DB 382 AADIDNSGTYDEFLAATLHMKMERETLVAASFDEKDGSGYITIDELQACATFGL 441
 QY 434 CDTPLDMKIDELDNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLFNFIADAFV 488
 DB 442 DDTIHDMKIDELDNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLFNFIADAFV 494

RESULT 2

CDPL_ATH STANDARD; PRT; 610 AA.
 AC Q06850;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Calcium-dependent protein kinase, isoform AK1 (EC 2.7.1.-) (CDPK).
 GN AK1 OR AT5G04870 OR MUK11.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=93213795; PubMed=7916621;
 RA Harper J.F., Binder B.M., Sussman M.R.;
 RT "Calcium and lipid regulation of an Arabidopsis protein kinase
 expressed in *Escherichia coli*.";
 RL Biochemistry 32:3282-3290(1993).
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;
 RX MEDLINE=98162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned pl clones.";
 RL DNA Res. 4:401-414(1997).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 CC INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
 CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
 CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN MOUSE-EAR
 CC CRESS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

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 CC or send an email to license@isb-sib.ch).

EMBL; L14771; AAA32761.1; -;
 EMBL; AB008271; BAB08991.1; -;
 DR F1R; A49082; A49082.
 DR HSP; P02588; IPON.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00336; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00018; EF_HAND; 4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Calcium-binding; Phosphorylation; Multigene family.
 FT DOMAIN 150 408
 FT NP_BIND 156 164
 FT BINDING 179 179
 FT ACT_SITE 274 274
 FT CA_BIND 464 475
 FT CA_BIND 500 511
 FT CA_BIND 536 547
 FT CA_BIND 570 581
 SQ SEQUENCE 610 AA; 68253 MW; 41868DF12B0DF9FB CRC64;

Query Match 66.5%; Score 1724; DB 1; Length 610;
 Best Local Similarity 65.5%; Pred. No. 2e-79;
 Matches 329; Conservative 62; Mismatches 91; Indels 20; Gaps 2;

QY 2 ETKP-----NPRRP-----SNTVLPQTPRLRDHYLLGKLGQGGFTY 41
 DB 106 ETKPESKPPPAKPKKPKMKRVSSAGLRTSVLQRTKFNKEFYSLGRKLGQGGFTT 165
 QY 42 LCTEKSTSNANYACKSIPKRLKVCREDYEDVWRVETQIMHLSHPNNVRIKGYEDSVVH 101
 DB 166 LCVEATGKEFAKSIARKLLTDDEVDVREIQIMHLSHPNNVRIKGYEDSVVH 225
 QY 102 IYMEYCEGELFDRIYKSGHFSERAVKLKTILGVWACHSLGVMHRLKPFNLFDS 161
 DB 226 LYMECCAGGELEDRILQIRGHYTERAAELTRTIVGVWACHSLGVMHRLKPFNLFVSK 285
 QY 162 KDAKALKATDFGLSVFYKPGQYLYDVGSPYYVAPEVLKCKYGPEDVWSAGVILYLLS 221


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RL Plant Mol. Biol. 27:953-967(1995).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X81394; CAA57157.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 85 343
FT NP_BIND 91 99 ATP (BY SIMILARITY).
FT BINDING 114 114 ATP (BY SIMILARITY).
FT ACT_SITE 209 209 BY SIMILARITY.
FT CA_BIND 398 409 EF_HAND 1 (POTENTIAL).
FT CA_BIND 434 445 EF_HAND 2 (POTENTIAL).
FT CA_BIND 470 481 EF_HAND 3 (POTENTIAL).
FT CA_BIND 505 516 EF_HAND 4 (POTENTIAL).
SQ SEQUENCE 533 AA; 59522 MW; D0BC570ABD289E28 CRC64;

Query Match
Best Local Similarity 61.3%; Score 1482; DB 1; Length 533;
Matches 284; Conservative 75; Mismatches 98; Indels 6; Gaps 3;

QY 4 KPNRRPSNTVLPQTPLRDLHYLLGKLGQGFQGTYYLCTEKTSTSNYACKSIPKRLV 63
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 KPTP-----DTILGLKYDDVRSVYSLGKELGRGQFGVTYLCFTEIASGKQYACKSISKRLV 122
QY 64 CREDYEDVWREIQIMHHLSEPNVVRIRKGTYESVVFHIVMCEGGELEFDRIYVSKGHFS 123
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
123 SKADKEDIRREIQIMHLSGQGNIVERGAYEDKSNVHVWELCAGGELFDRIIAKGHYS 182
QY 124 ERVAVKIKITLGVVACHSGVSHRDLKPNFLFDSPKDAKLKATDFGLSVFYKFGQY 183
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183 ERAAATICRAVVNVVNICHEFGVMHRLKPNFLLATKEENAMLKATDFGLSVFYEGKM 242
QY 184 LYDVVGSFYVAVPELVKKCYGPEIDVWSAGVILYLLSGVPPFAWETSGIFRILQGLK 243
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
243 YRDVGSAYVAVPEVRNRYGKEDVWSAGVILYLLSGVPPFAWETSGIFRILQGLK 302
QY 244 DFKSDPMTPTISEAAKDLIKMLSPKRRITSAHEALCHPWTVDSQAAPDKPLDPAVLSRL 303
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
303 DFESQWPESISEAKDLVRKMLTQDPKRRITSAQVLPWLRQGEAS-DKPDIDSAVLISM 361
QY 304 KQFSOMNKKKALVIAERLSEIEIGLKEFLKMDITDNSGTTTFEELKAGLRVGSSEL 363
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
362 KQFRAMNKKKALVIAERLSEIEIGLKEFLKMDITDNSGTTTFEELKAGLRVGSSEL 421
QY 364 MESIKSLMDAADNDSGTIDYGFELATLHNMKEREILVAAFSDFDKDGSYITIDE 423

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Db 422 SEAEVQLMEADVDGNSIDYVEFITATMRHKLDERHLFKAFQYDFDKNSGFTIRDE 481
QY 424 LOSACTEGLGDT-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 482 LESALIEHMGDTSTIKDIISVEDIDNDGRINYEFCAMMRGG 524

RESULT 5
CDP2_MAIZE
ID CDP2_MAIZE STANDARD; PRT; 513 AA.
AC P49101;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase 2 (EC 2.7.1.-) (CDPK 2).
GN CDPK2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Merrit; TISSUE=Root tip;
RA MEDLINE=95281563; PubMed=7761420;
RA Patil S., Takezawa D., Poovaiyah B.W.;
RA "Chimeric plant calcium/calmodulin-dependent protein kinase gene with
RA a neural visinin-like calcium-binding domain.";
RA Proc. Natl. Acad. Sci. U.S.A. 92:4897-4901(1995).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION
CC OF THE KINASE ACTIVITY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U28376; AAA69507.1; -.
DR HSSP; Q63450; 1A06.
DR MaizeDB; 56895; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation.
FT DOMAIN 65 323
FT NP_BIND 71 79 ATP (BY SIMILARITY).
FT BINDING 94 94 ATP (BY SIMILARITY).
FT ACT_SITE 189 189 BY SIMILARITY.
FT CA_BIND 379 390 EF_HAND 1 (POTENTIAL).
FT CA_BIND 415 426 EF_HAND 2 (POTENTIAL).
FT CA_BIND 451 462 EF_HAND 3 (POTENTIAL).
FT CA_BIND 486 497 EF_HAND 4 (POTENTIAL).

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DR SMART: SM00220: S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
FT Repeat.
FT DOMAIN 20 40 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X-
D-X.
FT REPEAT 20 26 1.
FT REPEAT 27 33 2.
FT REPEAT 34 40 3.
FT DOMAIN 148 410 PROTEIN KINASE.
FT NP_BIND 154 162 ATP (BY SIMILARITY).
FT BINDING 180 180 ATP (BY SIMILARITY).
FT ACT_SITE 276 276 BY SIMILARITY.
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 502 513 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 542 553 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT DOMAIN 574 585 ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
SQ SEQUENCE 602 AA; 67184 MW; 1D10BF68B37BF447 CRC64;
Query Match 32.9%; Score 854; DB 1; Length 602;
Best Local Similarity 41.2%; Pred. No. 5,1e-36;
Matches 184; Conservative 90; Mismatches 155; Indels 18; Gaps 8;
QY 28 LQKLGQGGFGTTLCTEKSSTANY-----ACKSTPKKLVCREDEDYVWREIQIMHLS 82
Db 150 VGEVGRGHFG--YTCRAKFKGEGKGDVAVKVPKAMITAIADVDVREVKILRALT 207
QY 83 EHPNVVRKGTVEDSVFHVMEVCEGELFDRIYSK-GHSESEAVKLITILGVVEAC 141
Db 208 GHNLVQVYDAFEDHTNVVMECEGELLDRILSRGKGTEDDAKAVMIOILNVAF 267
QY 142 HSLGVHRLDLPENLFDSPDKAKLTFGLSVFYKPGVLYDVVGSPPYVAPEVLK 201
Db 268 HLQGVVHRLDLPENLFLSKDSDSOLKAIDFGLSDYVVPDLNDIVGSYYVAPEVL 327
QY 202 CYGPIDVWSAGVILYIILLGVPVPWATESGIFRQILQGLDKFSDWPITSEAKDL 261
Db 328 SYSTFADVWSIGVSYILLGSRPWPATESGIFRAVILKANLSFDPFPWPVSSSEAKDF 387
QY 262 YKMLERSPKKRISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSQMNKKKMLARV 321
Db 388 KRLNKKDPKRTAAQALCHSWIKNSNDI-KFPLDILVFLKMKVYRSPLEKALRAL 446
QY 322 EELSEETGGELKFKMIDTDSNGTITTEELKAGLKRGVSELM-ESETKSLMDAADIND 380
Db 447 KTLTVDELFLYKEQFVLEPTKNGTISLENIKQALMRNSTAMKDSRVLVLSNALQY 506
QY 381 GTIDYGEFLAATLHNMKMER----EELVAAFSDFDKGSGVITIDELQSACTERGLCD 436
Db 507 RMDFEEFCAALSVHQLEALDRWEQHARCAVDLFEKDGNRIMTEELAS---ELGLGFS 563
QY 437 -PLDMIKIEDLDNDGKIDFSEFTAMM 462
Db 564 IPVHAVLHDWIRHTDGLKSLFLGYVKLL 590

RESULT 9

KCCD_HUMAN STANDARD; PRT; 499 AA.
AC Q13557; Q9UQE9; Q9UGH6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC 2.7.1.123) (Cam-kinase II delta chain) (Cam kinase II delta subunit) (CaMK-II delta subunit).
DE (Human).
GN CAMK2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.
RP TISSUE-Myocardium;
RX MEDLINE=99205154; PubMed=10189359;
RA Hoch B., Meyer R., Hetzer R., Krause E.-G., Karczewski P.;
RT "Identification and expression of delta-isoforms of the
RT multifunctional Ca2+/calmodulin-dependent protein kinase in failing
RT and nonfailing human myocardium.";
RL Circ. Res. 84:713-721(1999).
RN [2]
RP SEQUENCE OF 1-243 FROM N.A.
RC TISSUE-Insulinoma;
RA Rochlitz H., Voigt A., Lankat-Buttgereit B., Goetze B., Heimberg H.,
RA Nauck M.A., Schiemann U., Schatz H., Pfeiffer A.;
RT "Cloning of the human calcium/calmodulin dependent protein kinase II
RT isoforms in human beta cells.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 302-417 FROM N.A.
RX MEDLINE=97214519; PubMed=9060999;
RA Tombes R.M., Krystal G.W.;
RT "Identification of novel human tumor cell-specific CaMK-II variants.";
RL Biochim. Biophys. Acta 1355:281-292(1997).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: DELTA 1, DELTA 2 (SHOWN HERE),
CC DELTA 3, DELTA 4, DELTA 8, DELTA 9; ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CARDIAC MUSCLE AND SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

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EMBL; AF071569; AAD20442.1; -;
EMBL; AJ252239; CAB65123.1; -;
EMBL; U50361; AAB16866.1; -;
HSSP; Q63450; 1A06.
Genew; HGNC:1462; CAMK2D.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Neurone; Alternative splicing.
FT DOMAIN 14 272 PROTEIN KINASE.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
FT CONFLICT 39 39 G->E (IN REF. 2).
SQ SEQUENCE 499 AA; 56297 MW; BBEF05669A883E65 CRC64;
Query Match 22.8%; Score 591; DB 1; Length 499;
Best Local Similarity 37.1%; Pred. No. 5,4e-23;
Matches 142; Conservative 65; Mismatches 144; Indels 32; Gaps 9;

QY 21 RLDRHLLGKLGQGGFGTTLCTEKSSTANYACKSTPKKLVCREDEDYVWREIQIMH 80

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Db 9 RTDEYQLFEELGKGAFSVVRRCMKIPTQGGYAAKLIINTKKLSAR-DHOKLEREARIC-R 66
QY 81 LSEHPNVVRIKGTIYEDSVFHVIMEVCEGELFDRIYVSKGHFSEAEVAVKLITILGVVEA 140
Db 67 LLKHPNIVRLHDSISFEGFHYLVDFDLVGTGELFDIVAREYVSEADASHCIQIILSVNH 126
QY 141 CHSLGVNHRDLKPNFLFSPKDDAKLKTATDFGLSVFYKPGQYL-YDVVGSYYVAPEVL 199
Db 127 CHLNGIVHRDLKPNILLASKSGAAVKLADEGLALEVQDQOQAWFGEAGTGYLSPEVL 186
QY 200 KK-CYGPETDVSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWPTISEAAK 258
Db 187 KDPYKGVDMWACGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWPTISEAAK 246
QY 259 DLIYKMLSPKRRISAEALCHPWTVDQAAAPDKPLDPFAVLSRLKQFSOMNKKIKMALR 318
Db 247 DLINKMLTINPAKRITASEALKHPWCICQSTVASMHRQETVDCLKKFNARRKLKG---A 303
QY 319 VTAERLSEREIGLKLPMID-----TNSG-TITFEELKA---GLKRVGSELMSEIK 369
Db 304 ILTMTLATRNSAASLLKPKDGVKSTESNTTIEDVDKARKQBIKVTQOLIEA--- 360
QY 370 SLMDAADIDNSGIDYGEFLAAT 392
Db 361 -----INNGDFEAYT 370

RESULT 10
KCCL_RAT
ID KCCL_RAT STANDARD; PRT; 374 AA.
AC Q63450; Q63084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (37 KDA ISOFORM).
RX MEDLINE=94075341; PubMed=8253780;
RA Picciotto M.R., Czernik A.J., Nairn A.C.;
RT "Calcium/calmodulin-dependent protein kinase I. cDNA cloning and
RT identification of autophosphorylation site.";
RL J. Biol. Chem. 268:26512-26521(1993).
RN [2]
RP SEQUENCE FROM N.A. (42 KDA ISOFORM).
RC STRAIN-Sprague-Dawley; TISSUE=Lung;
RX MEDLINE=95035115; PubMed=7948038;
RA Cho F.S., Phillips K.S., Bogucki B., Weaver T.E.;
RT "Characterization of a rat cDNA clone encoding calcium/calmodulin-
RT dependent protein kinase I.";
RL Biochim. Biophys. Acta 1224:156-160(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF SHORT FORM.
RC TISSUE=Brain;
RX MEDLINE=96182648; PubMed=8601311;
RA Goldberg J., Nairn A.C., Kuriyan J.;
RT "Structural basis for the autoinhibition of
RT calcium/calmodulin-dependent protein kinase I.";
RL Cell 84:875-887(1996).
CC -!- FUNCTION: PHOSPHORYLATES SYNAPSIN I.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-Phosphoprotein.
CC -!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
CC PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

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CC -----
DR EMBL; L24907; AAA19670.1; -
DR EMBL; L26288; AAA66944.1; -
DR PDB; 1A06; 08-APR-98.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Alternative splicing; 3D-structure.
FT DOMAIN 20 276
FT CALMODULIN-BINDING (BY SIMILARITY).
FT BINDING 26 34
FT NP_BIND 26 34
FT BINDING 49 49
FT ACT_SITE 141 141
FT MOD_RES 177 177
FT VARSPPLIC 323 374
FT FT
FT CONFLICT 112 112 F -> G (IN REF. 1).
FT CONFLICT 118 118 A -> R (IN REF. 1).
FT CONFLICT 309 309 A -> R (IN REF. 1).
FT SEQUENCE 374 AA; 41638 MW; 37889B3DEF033AB2 CRC64;
SQ
Query Match 22.7%; Score 589.5; DB 1; Length 374;
Best Local Similarity 41.6%; Pred. No. 4.7e-23;
Matches 124; Conservative 56; Mismatches 113; Indels 5; Gaps 4;
QY 18 QTPRLRDHYLLGKLGQGGTGYLTCTEKSTANYACKSIPKRLKVCREDYDWEIQL 77
Db 12 QAEDIRDIYDFRDLGTGAFSEVILAEDEKFTQKLVAIKCIAKKALEGKEG--SMENEIAV 69
QY 78 MHLSEHPNVVRIKGTIYEDSVFHVIMEVCEGELFDRIYVSKGHFSEAEVAVKLITILGV 137
Db 70 LHKI-KHPNIVALDDIYESGHHYILNGLVSGGELFDRIYVEKGFYTERDASRLIFQVLD 128
QY 138 VEACHSLGVNHRDLKPNFLFSPKDDAKLKTATDFGLSVFYKPGQYLVDVVGSPYYVAPE 197
Db 129 VKYLHDLGIVHRDLKPNFLFSPKDDAKLKTATDFGLSVFYKPGQYLVDVVGSPYYVAPE 188
QY 198 VL-KKCYGPELDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWPTISEA 256
Db 189 VLAQKPYKSAVDQMSIGVIAYIILCGYPFYDENDAKLFEQILKAEYEFDSPTWDDISDS 248
QY 257 AKDLIYKMLSPKRRISAEALCHPWTVDQAAAPDKPLDPFAVLSRLKQFSOMNKKIK 314
Db 249 AKDFIRHLMKDEPKRFTCEQALQHPWIAQDTAL-DKNIHQSVSEQLKKKFAKSKWKQ 305
RESULT 11
KCCL_HUMAN
ID KCCL_HUMAN STANDARD; PRT; 370 AA.
AC Q14012;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95369239; PubMed=7641687;
RA Haribabu B., Hook S.S., Seibert M.A., Goldstein E.G., Tomhave E.D.,
RT Edelman A.M., Snyderman R., Means A.R.;
RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,
RT domain structure and activation by phosphorylation at threonine-177
RT by calcium-calmodulin dependent protein kinase I kinase.";
RL EMBL J. 14:3679-3686(1995).
CC -!- FUNCTION: PHOSPHORYLATES SYNAPSIN I.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
CC PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC -!- SUBUNIT: MONOMER.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L41816; AAA99458.1; -.
CC HSP; Q63450; IAO6.
CC Genew; HGNC:1459; CAMK1.
CC MIM; 604998; -.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
CC Phosphorylation; ATP-binding; Alternative splicing.
FT DOMAIN 20 276 PROTEIN KINASE.
FT DOMAIN 287 321 CALMODULIN-BINDING (BY SIMILARITY).
FT NP_BIND 26 34 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP.
FT ACT_SITE 141 141 BY SIMILARITY.
FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-).
FT MUTAGEN 49 49 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 370 AA; 41337 MW; 57FA20CEG0FA76C CRC64;
Query Match 22.7%; Score 587.5; DB 1; Length 370;
Best Local Similarity 41.6%; Pred. No. 5.9e-23;
Matches 124; Conservative 55; Mismatches 114; Indels 5; Gaps 4;
QY 18 QTPRLRDHYLLGKLGQGFQGTLYCTEKSTKSANYACKSIPKRLVCRVEDYEDVWREIQI 77
DB 12 QAEIRDYIDFDVDTGAFSEVILAEKRTQKUNIAIKAEALGEG--SMENEIATV 69
QY 78 MHLSEHPNVRIKGYEDSVFHVIMEYCEGGEFLDRIVSKGHFSEREAVKLITILGV 137
DB 70 LHKI-KHPNIVALDDIYSGGHLXLMQLVSGGELDFRIVEKGFYTERDASRLIFQVLD 128
QY 138 VFACHSLGVNHRDLKPNELFSPKDDAKLKATDFGLSVFYKPGQVLYDVGVSPYVAPE 197
DB 129 VKYLDLGLVHVRDLKPNELLYXSLDEDSKIMLSDFGLSKMEDPGSVLSTACGTPGYAPE 188
QY 198 VL-KKCYGEIDVWAGVLYLTLSSVPPFWAETESGIFRILQCKLDFKSDPWTISEA 256
DB 189 VLAQPKYKAVCWSTIGVYATILLCGYPPFYDENAKLFEQILKAEYFDPSPYWDIDIS 248
QY 257 AKDLIVKMLERSPKKRISAEALCHFPWIVDEQAAPKPLDPAVLGRKQFOSMNKIKK 314
DB 249 AKDFIHLMEKDPKRFTECEALQHPHTWAGTDAL-DKNHQSVSQIKKFNFAKSKWKQ 305
```

RESULT 12

KCC4_HUMAN STANDARD; PRT; 473 AA.

AC Q16566;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain

DE (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV).

GN CAMK4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94375404; PubMed=8089075;

RA Kitani T., Okuno S., Fujisawa H.;

RT "cDNA cloning and expression of human calmodulin-dependent protein

RT kinase IV.";

RL J. Biochem. 115:637-640(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX TISSUE=Cerebellum, and Thymus;

RX MEDLINE=94252566; PubMed=8194751;

RA Bland M.M., Monroe R.S., Ohmsted C.A.;

RT "The cDNA sequence and characterization of the

RT Ca2+/calmodulin-dependent protein kinase-Gr from human brain and

RT thymus.";

RN Gene 142:191-197(1994).

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Blood;

RX MEDLINE=94149862; PubMed=8107230;

RA Mosialos G., Hanissian S.H., Jawahar S., Vara L., Kieff E.;

RA Chatila T.A.;

RT "A Ca2+/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed

RT after transformation of primary human B lymphocytes by Epstein-Barr

RT virus (EBV) is induced by the EBV oncogene LMP1.";

RL J. Virol. 68:1697-1705(1994).

RN [4]

RP SEQUENCE FROM N.A.

RX TISSUE=Brain;

RA Strausberg R.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING

CC PROTEIN.

CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.

CC -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL

CC NUCLEI (BY SIMILARITY).

CC -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE

CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE

CC SPLICING.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CAMK SUBFAMILY.

CC -----

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CC -----

EMBL; D30742; BAA06403.1; -.

EMBL; L17000; AAA35639.1; -.

EMBL; L24959; AAA18251.1; -.

EMBL; BC016695; AAH16695.1; -.

HSP; Q63450; IAO6.

Genew; HGNC:1464; CAMK4.

MIM; 114080; -.

```

DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding.
FT DOMAIN 46 300 PROTEIN_KINASE.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT DOMAIN 322 341 CALMODULIN-BINDING (POTENTIAL).
SQ SEQUENCE 473 AA; 51925 MW; 5FE5E15612326DC CRC64;

Query Match 22.3%; Score 578.5; DB 1; Length 473;
Best Local Similarity 37.2%; Pred. No. 2.1e-22;
Matches 140; Conservative 65; Mismatches 144; Indels 27; Gaps 10;

QY 22 LRHYLGKKGQGGFTYCTEKTSTANYACKSIPKRLVCREDEDVWREIQIMHHL 81
DB 42 LSDFEVESELGRGATSIYVRCKQGTQKPYALKVLAK-----TVDKKIVRTIEIGVLLRL 96
QY 82 SEHPNVVRKIGTYEDSVFVHTVMEVCEGGELFDRIIVSGHSEAEVAKLTKILGVVEAC 141
DB 97 S-HENIKRLKEIFPTPEISLVLSVLTGGELFDRIIVSGYSEDAVAKQIILEAVYL 155
QY 142 HSLGVMRDLKPNFLDFSPKDDAKLTKATDGLSVFVKPGQYLDVVGSPYVVAPEVLKK 201
DB 156 HENGIVHRDLKPNLLYATPAPDAPLAKIADGLSKIVHEQVLMKTVCSTPGYCAPEILRG 215
QY 202 C-YGPEIDVWSAGVILLISGVPPFWAET-ESGIFRQIQLOGKLDKPSDPWPTTSEAAKD 259
DB 216 CAYGPEVDMWSGVITILLGCGFFYDERGDFMFRILNCEYFIFFSPWDEVSNAKD 275
QY 260 LIYKMLERSPKRISAEALCHPWVDEQAAPDKPLDPAVLSRLKQFSOMNKKIKMALRV 319
DB 276 LVRLKIVLDPKRLTTFQALQHPWTVG-KAANFVHMDTA-QKQLQFNARKRLKAAVYKAV 333
QY 320 IA-BRL-SEEEIGLKLFLFKM-----IPDINSGTITFEF-----LKAGLKRGVSE 362
DB 334 VASSRLGSASSSHGSIQESHKASRDSPPIQDGNEDMKAIPGERIQDGAQAAYKGAQAE 393
QY 363 LMESEIKSLMDAADID 378
DB 394 LMKVQALEKVKGADIN 409

RESULT 13
KCCD_RAT STANDARD; PRT; 533 AA.
AC P15791;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC
DE 2.7.1.123) (Cam-kinase II delta chain) (Cam kinase II delta subunit)
DE (CaMK-II delta subunit).
GN CAMK2D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
EN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90036861; PubMed=2553697;
RA Tobimatsu T., Fujisawa H.;
RT "Tissue-specific expression of four types of rat calmodulin-dependent
RT protein kinase II mRNAs.";
RL J. Biol. Chem. 264:17907-17912(1989).
DB [2]

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RP SEQUENCE OF 314-533 FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Aorta, and Skeletal muscle;
RA MEDLINE=93300844; PubMed=8390994;
RX Schworer C.M., Rothblum L.I., Thekkumkara T.J., Singer H.A.;
RT "Identification of novel isoforms of the delta subunit of
RT Ca2+/calmodulin-dependent protein kinase II. Differential expression
RT in rat brain and aorta.";
RL J. Biol. Chem. 268:14443-14449(1993).
CC -1- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -1- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; DELTA 1 (SHOWN HERE), DELTA 2,
CC DELTA 3 AND DELTA 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: DELTA 1 IS THE PREDOMINANT FORM IN THE
CC BRAIN, DELTA 2 AND 3 PREDOMINATE IN THE AORTA AND DELTA 4
CC IN SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC -----
DR EMBL: J05072; AAA40866.1; -
DR EMBL: L13406; AAA41479.1; -
DR EMBL: L13407; AAA41480.1; -
DR EMBL: L13408; AAA41481.1; -
DR HSP: Q63450; A34366.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Neurone; Alternative splicing.
FT DOMAIN 14 272 PROTEIN_KINASE.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
FT VARSPLIC 329 362 MISSING (IN ISOFORM DELTA 2).
FT VARSPLIC 329 335 INKANV -> KRKSSV (IN ISOFORM DELTA 3).
FT VARSPLIC 337 359 MISSING (IN ISOFORM DELTA 3).
FT VARSPLIC 360 362 GNK -> QMM (IN ISOFORM DELTA 3).
FT VARSPLIC 349 362 MISSING (IN ISOFORM DELTA 4).
SQ SEQUENCE 533 AA; 60080 MW; E41BCB2B5A00E7CA CRC64;

Query Match 22.2%; Score 574.5; DB 1; Length 533;
Best Local Similarity 39.4%; Pred. No. 3.8e-22;
Matches 127; Conservative 54; Mismatches 134; Indels 7; Gaps 5;

QY 21 RLRDHYLGKKGQGGFTYCTEKTSTANYACKSIPKRLVCREDEDVWREIQIMHH 80
DB 9 RFTDEYQLFEELGKGFVVRRCMKIPTGOEYAAKIINTKKLSAR-DHOKLEEARIC-R 66
QY 81 LSEHPNVVRKIGTYEDSVFVHTVMEVCEGGELFDRIIVSGHSEAEVAKLTKILGVVEA 140
DB 67 LLKHPNIVRLHDSISEEGFHYLVDPDLVTGGELFDRIIVAREYSEADASHGCIQILESVNH 126
QY 141 CHSGYVMHRDLKPNFLDFSPKDDAKLTKATDGLSVFVKPGQYL-YDVVSGSPYVVAPEVL 199
DB 127 CHLNGIVHRDLKPNLLYATPAPDAPLAKIADGLSKIVHEQVLMKTVCSTPGYCAPEILRG 186

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RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
RX MEDLINE=91288548; PubMed=1648230;
RA Ohmsted C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
RL kinase Gr and caldespermin: a gene within a gene";
RN proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=91304387; PubMed=1649385;
RA Means A.R., Cruzalegui F., Lemaquerresse B., Needleman D.S.,
RA Slaughter G.R., Ono T.;
RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
RT cell-specific calmodulin-binding protein are derived from the same
RL gene.";
RN Mol. Cell. Biol. 11:3960-3971(1991).
RP SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=89174647; PubMed=2538431;
RA Ohmsted C.-A., Jenson K.F., Sahyoun N.;
RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
RT granule cells. Identification of a novel neuronal
RT calmodulin-dependent protein kinase.";
RN J. Biol. Chem. 264:5866-5875(1989).
RP SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=89123272; PubMed=2914893;
RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;
RT "Molecular cloning sequence and distribution of rat caldespermin, a
RT high affinity calmodulin-binding protein.";
RN J. Biol. Chem. 264:2081-2087(1989).
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=96094352; PubMed=7493991;
RA Sun Z., Means R.B., Lemaquerresse B., Means A.R.;
RT "Organization and analysis of the complete rat calmodulin-dependent
RT protein kinase IV gene.";
RN J. Biol. Chem. 270:29507-29514(1995).
CC -!- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
CC ENRICHED IN CEREELLAR GRANULE CELLS.
CC -!- FUNCTION: CALDESPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/calcium-calmodulin-dependent
CC protein kinase type IV catalytic chain (shown here) and
CC 2/calspermin; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2
CC is testis-specific.
CC -!- PTM: THE N-TERMINAL OF CALDESPERMIN IS BLOCKED.
CC -!- MISCELLANEOUS: The presence of an alternative promoter gives rise
CC to the testis-specific isoform 2/calspermin protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M63334; AAA0865.1; -
CC DR EMBL; M74488; AAA0845.1; ALT_SEQ.
CC DR EMBL; M64757; AAA0856.1; -
CC DR EMBL; M64757; AAA0857.1; -
CC DR EMBL; J04600; AAA1867.1; -
CC DR EMBL; J04446; AAA0990.1; -
CC DR PIR; A41103; TVRTC4.
CC HSSP; O63450; 1A06.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.

PFam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding; Testis; Alternative splicing.
FT DOMAIN 42 296 PROTEIN KINASE.
FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT BINDING 71 71 BY SIMILARITY.
FT ACT_SITE 160 160 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 318 337 POLY-GLU.
FT DOMAIN 393 399 POLY-GLU.
FT DOMAIN 403 413 MISSING (IN ISOFORM 2).
FT VARSPPLIC 1 305 I -> M (IN REF. 2 AND 4).
FT CONFLICT 372 372 56F7AC5644DED23 CRC64;
SQ SEQUENCE 474 AA; 53133 MW; 56F7AC5644DED23 CRC64;
Query Match 22.1%; Score 572; DB 1; Length 474;
Best Local Similarity 34.1%; Pred. No. 4.5e-22;
Matches 142; Conservative 75; Mismatches 158; Indels 42; Gaps 11;
QY 3 TKPN-PRPSNTVLPYQTPRLRDHYLLGKK-----LGQGFQGTYYLCTEKST 48
DB 5 TVPSCPSPSCSSVTSSTENLVPDWDGSKRDPLSDFFVESELGSGATSIYRCKQKGT 64
QY 49 SANYACKSIPKRLKVCREDYEDVWREIQIMHLSHPNVVRIKTYEDSVFVHIVEYCE 108
DB 65 OKPYAKVLKK-----TVDKKIVRTIGVLLRLS-HPNIIKKEIFETPTETISIVLELV 118
QY 109 GGELFDRIYVSKGHFSEERAVKLITKILGVVEACHSLGVWHRDLKPEFLDPSKDDAKLK 168
DB 119 GGELFDRIYVSKGHFSEERAVKLITKILGVVEACHSLGVWHRDLKPEFLDPSKDDAKLK 178
QY 169 ATDFGLSVFYKPGQYLYDVGVSPYYVAPEVLKCC-YGPEIDVWVGAGVILYILLGVPPFW 227
DB 179 IADFGLSKIVEHQVLMKTVCGTGYCAPELLRGCAYGPEVDMWSVGIIITYILGFEFFY 238
QY 228 AET-ESGIFRQILQGLDFKDPWPTISEAAKDLIYKMLERSPKKRISAHALCHPWIVD 286
DB 239 DERGDQFMFRILNCEYYFISFWNDEVSLNAKDLVKKLIVLDPKRLTTFQALQHPWVTG 298
QY 287 EQAAPDKPLDPAVLRLKQFSQNMKIKKWLRLVIAERLSEEEIGGLKELFKMIDTDSGT 346
DB 299 KAANFVIMDTA-QKLOEFFNARRKLKAAVAVVA---SSPLGSSASSSHNIQESNKAS 352
QY 347 ITFEEKAGLKRKVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMKNMREEI 403
DB 353 SEAPQADGDKK--TDPLENKIQA-----GDHEAAKAAADETMKLQSEEV 395
Search completed: March 26, 2003, 13:10:50
Job time : 25 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 12:08:22 ; Search time 75 Seconds
(without alignments)
1359.911 Million cell updates/sec

Title: US-09-848-806-1
Perfect score: 2593
Sequence: 1 METKPNRRPSNTVLPYQTP.....KNLNFNIADAFVGDEKSD 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_prodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteria.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	Q39016	Q39016 arabidopsis
2	2577	99.4	495	Q949p0	Q949p0 arabidopsis
3	2536	97.8	557	Q91QH7	Q91QH7 arabidopsis
4	2458	94.8	501	Q38869	Q38869 arabidopsis
5	2030	78.3	490	Q24430	Q24430 glycine max
6	1969.5	76.0	496	Q93X19	Q93X19 solanum tub
7	1844.5	71.1	490	Q42396	Q42396 arabidopsis
8	1773	68.4	551	Q9FXQ3	Q9FXQ3 oryza sativ
9	1752	67.6	492	Q04417	Q04417 zea mays (m
10	1751	67.5	487	Q43676	Q43676 phaseolus a
11	1745	67.3	554	Q04123	Q04123 zea mays (m
12	1742	67.2	556	Q38871	Q38871 arabidopsis
13	1739.5	67.1	578	Q93XJ0	Q93XJ0 solanum tub
14	1733.5	66.9	578	Q93YF3	Q93YF3 nicotiana t
15	1731	66.8	544	Q38872	Q38872 arabidopsis
16	1728	66.6	581	Q93YF4	Q93YF4 nicotiana t

17	1719	66.3	646	10	Q38870	Q38870 arabidopsis
18	1717.5	66.2	578	10	Q24460	Q24460 tortula rur
19	1709.5	65.9	573	10	Q38838	Q38838 cucurbita p
20	1709	65.9	483	10	Q39014	Q39014 arabidopsis
21	1708	65.9	581	10	Q93YF7	Q93YF7 nicotiana b
22	1700.5	65.6	484	10	Q9S2M3	Q9S2M3 arabidopsis
23	1672.5	64.5	639	10	Q82107	Q82107 zea mays (m
24	1640.5	63.3	583	10	Q9ZV15	Q9ZV15 arabidopsis
25	1630	62.9	451	10	Q41789	Q41789 zea mays (m
26	1592	61.4	542	10	Q9SNK9	Q9SNK9 oryza sativ
27	1587	61.2	542	10	Q65003	Q65003 oryza sativ
28	1531.5	59.1	548	10	Q9S7Z4	Q9S7Z4 marchantia
29	1524.5	58.8	548	10	Q8S786	Q8S786 marchantia
30	1509.5	58.2	528	10	Q8VYE7	Q8VYE7 arabidopsis
31	1506.5	58.1	528	10	Q9FMP5	Q9FMP5 arabidopsis
32	1484.5	57.3	540	10	Q81390	Q81390 nicotiana t
33	1482	57.2	531	10	Q949U0	Q949U0 arabidopsis
34	1482	57.2	531	10	Q9ZSA2	Q9ZSA2 arabidopsis
35	1480	57.1	518	10	Q9AXA7	Q9AXA7 oryza sativ
36	1480	57.1	531	10	Q41790	Q41790 zea mays (m
37	1475	56.9	347	10	Q941Q5	Q941Q5 psophocarpu
38	1473	56.8	553	10	Q8RW36	Q8RW36 lycopersico
39	1471.5	56.7	521	10	Q94KH6	Q94KH6 lycopersico
40	1469.5	56.7	542	10	Q9AR92	Q9AR92 medicago sa
41	1464.5	56.5	514	10	Q9ARI5	Q9ARI5 cucumis sat
42	1463.5	56.4	521	10	Q9C6P3	Q9C6P3 arabidopsis
43	1462	56.4	529	10	Q42479	Q42479 arabidopsis
44	1462	56.4	534	10	Q9FRK2	Q9FRK2 oryza sativ
45	1458.5	56.2	538	10	Q24431	Q24431 glycine max

ALIGNMENTS

RESULT 1

Q39016	PRELIMINARY;	PRT;	495 AA.
ID	Q39016		
AC	Q39016;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Calcium-dependent protein kinase.		
GN	ACDPK2.		
OS	Arabidopsis thaliana (Mouse-ear cross).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=COLUMBIA;		
RX	MEDLINE=94959455; PubMed=8078458;		
RA	Urao T., Katagiri T., Mizoguchi T., Yamaguchi-Shinozaki K.,		
RA	Hayashida N., Shinozaki K.;		
RT	"Two genes that encode Ca2+-dependent protein kinases are induced by		
RT	drought and high-salt stresses in Arabidopsis thaliana.";		
RL	Mol. Gen. Genet. 244:331-340(1994).		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL; D21806; BAA04830.1; -		
DR	HSSP; P02593; 1FW4.		
DR	InterPro; IPR002048; EF-hand.		
DR	InterPro; IPR00719; Euk_pkinase.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	Pfam; PF00036; ehand; 4.		
DR	Pfam; PF00069; pkinase; 1.		
DR	ProDom; PD000001; Euk_pkinase; 1.		
DR	ProDom; PD000012; EF-hand; 2.		
DR	SMART; SM00054; Efh; 4.		
DR	SMART; SM00220; S_TKc; 1.		
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_4.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.		
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 495 AA; 55867 MW; 5909A451242CA6D CRC64;

Query Match 100.0%; Score 2593; DB 10; Length 495;
Best Local Similarity 100.0%; Pred. No. 9.5e-183;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
DB 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
QY 61 KLVCREDEYDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
DB 61 KLVCREDEYDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
QY 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180
QY 181 GOYLYDVGSPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB 181 GOYLYDVGSPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
QY 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
DB 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
QY 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
DB 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYYT 420
DB 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYYT 420
QY 421 IDELQSACTEFGCLDTPLDMDIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTMMKNLNF 480
DB 421 IDELQSACTEFGCLDTPLDMDIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTMMKNLNF 480
QY 481 NIADAFGVGDKESDD 495
DB 481 NIADAFGVGDKESDD 495

RESULT 2
Q949P0 PRELIMINARY; PRT; 495 AA.

AC Q949P0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative calcium-dependent protein kinase SK5.
GN F1504.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kaniya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.,
RT "Full length cDNA of gene F1504.8 (GI:8778378)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050981; AAK93658.1;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR PROSITE; PS00018; EF-hand; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 495 AA; 55916 MW; 2DD0ED8C234EF27 CRC64;

Query Match 99.4%; Score 2577; DB 10; Length 495;
Best Local Similarity 99.6%; Pred. No. 1.4e-181;
Matches 493; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
DB 1 METKPNRPSTNVLPTQPRLDHYLLGKLGKGGGFGTTLCTEKSTANTACKSIPKR 60
QY 61 KLVCREDEYDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
DB 61 KLVCREDEYDVREIOMHHLSEHPNVRKGTIYEDSVFVHIVMEYCEGGELEFDRIVSKG 120
QY 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPENLFDSPKDDAKLKATDFGLSVFYKP 180
QY 181 GOYLYDVGSPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB 181 GOYLYDVGSPYVAPEVLKCKYCPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
QY 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
DB 241 GKLDKSDPWTPTTISEAAKOLLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYL 300
QY 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
DB 301 SRLKQFSQMNKIKKMLRVTAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVKG 360
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYYT 420
DB 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYYT 420
QY 421 IDELQSACTEFGCLDTPLDMDIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTMMKNLNF 480
DB 421 IDELQSACTEFGCLDTPLDMDIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTMMKNLNF 480
QY 481 NIADAFGVGDKESDD 495
DB 481 NIADAFGVGDKESDD 495

RESULT 3
Q91QH7 PRELIMINARY; PRT; 557 AA.

AC Q91QH7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F1504.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;

Submitted (OCT-1999) to the EMBL/GenBank/DBDJ databases.

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RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altai H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thayer A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBDJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC007887; AAF79386.1; -.
DR HSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 557 AA; 63397 MW; 7E92BA5A6B3A240B CRC64;

Query Match 97.8%; Score 2536; DB 10; Length 557;
Best Local Similarity 88.5%; Pred. No. 1.8e-178;
Matches 493; Conservative 0; Mismatches 17; Indels 62; Gaps 1;

QY 1 METKPNRPSTNVLPTQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIKPR 60
Db 1 METKPNRPSTNVLPTQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIKPR 60

QY 61 KLVCRDEYDWMREIQIMHLSHEPNVRIKGTYESVVFHIVMEVCEGGEFLDRIVSKG 120
Db 61 KLVCRDEYDWMREIQIMHLSHEPNVRIKGTYESVVFHIVMEVCEGGEFLDRIVSKG 120

QY 121 HFSREAVKLITLGVVEACHSLGVHMDLKPENFLDSPKDDAKLATDGLSVFYKPR 180
Db 121 HFSREAVKLITLGVVEACHSLGVHMDLKPENFLDSPKDDAKLATDGLSVFYKPR 180

QY 181
Db 181 GLIIFLWLIDSLILQLFWLFFVSMNRKLKQSGFLIETGLLCFIWIANRNKVFQMYRFD 240

QY 181 --GQYLVDVWGSPYVAVPEVLKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQI 238
Db 241 LEGQYLVDVWGSPYVAVPEVLKCKYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQI 300

QY 239 LOGKLDKSDPWTPTISEAAKOLYIKMLERSPKKRISAHEALCPHWIVDEQAAPDKPLDPA 298
Db 301 LOGKLDKSDPWTPTISEAAKOLYIKMLERSPKKRISAHEALCPHWIVDEQAAPDKPLDPA 360

QY 299 VLSRLKQFSQMNKIKKMLRVIAERLSEIEIGLKLKFMIDTNSGTTTFPEELKAGLKR 358
Db 361 VLSRLKQFSQMNKIKKMLRVIAERLSEIEIGLKLKFMIDTNSGTTTFPEELKAGLKR 420

QY 359 VGSSELMSEIKSLMDAADTNSGTTIDYGEFLAATLHMKNKWEREELVAFSDFDKDGSY 418
Db 421 VGSSELMSEIKSLMDAADTNSGTTIDYGEFLAATLHMKNKWEREELVAFSDFDKDGSY 480

QY 419 ITIDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKKGVGGRSRTMKNL 478
Db 481 ITIDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKKGVGGRSRTMKNL 540

QY 479 NFNIADAFGVGGEKSD 495
Db 541 NFNIADAFGVGGEKSD 557
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RESULT 4
Q38869 PRELIMINARY; PRT; 501 AA.
AC Q38869;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Calmodulin-domain protein kinase CDPK isoform 4 (Fragment).
GN CPK4 OR T25P22.10 OR AT4G09570.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RA McCombie W.R.;
RT "Arabidopsis thaliana Genomic Sequence, Chromosome IV.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBDJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA McCombie R.W., Spiegel L.A., Huang E.N., Nascimento L.U.,
RA de la Bastide M., Vil D.M., Preston R.R., Matro A., Shah R.,
RA O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H.,
RA Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBDJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matro A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBDJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31752; AA803243.1; -.
DR EMBL; AL161831; CAB82124.1; -.
DR EMBL; AL161515; CAB78080.1; -.
DR HSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 501 AA; 56416 MW; C709C17DEAF74B70 CRC64;

Query Match 94.8%; Score 2458; DB 10; Length 501;
Best Local Similarity 94.8%; Pred. No. 8.6e-173;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRRPSTNVLPTQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIKPRKLV 63
Db 3 KPNRRPSTNVLPTQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIKPRKLV 62

QY 64 CREDYEDVWREIQIMHLSHEPNVRIKGTYESVVFHIVMEVCEGGEFLDRIVSKGCF 123
Db 63 CREDYEDVWREIQIMHLSHEPNVRIKGTYESVVFHIVMEVCEGGEFLDRIVSKGCF 122
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Query Match 78.3%; Score 2030; DB 10; Length 490;
 Best Local Similarity 81.1%; Pred. No. 2.8e-141;
 Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;

QY 14 VLVPQPRLDHYLGLKKGQGGTTLCTEKSTANYACKSIPKRLKVCREDYEDVWR 73
 DB 12 VLVPQARLDHYLGLKKGQGGTTLCTHKVTKLYACKSIPKRLKVCREDYEDVWR 71
 QY 74 EIQIMHLSHPPNVRIKGTEDSVFVHYVMEVCEGELEFDRIVSKGHSEFAVKLIT 133
 DB 72 EIQIMHLSHPPNVQIQGTEDSVFVHYVMEVCEGELEFDRIVSKGHSEFAVKLIT 131
 QY 134 ILGVVEACHSLGVNHRDLKPNFLFDSKPKDAKAKATDFGLSVFKPGQVLYDVVGSPPY 193
 DB 132 ILGVVEACHSLGVNHRDLKPNFLFDSKPKDAKAKATDFGLSVFKPGQVLYDVVGSPPY 191
 QY 194 VAPVLAACKYGPETDVMSAGVILYLLSGVPPFAETESGIFRQILQKLFDFKSDPWPTI 253
 DB 192 VAPVLAACKYGPETDVMSAGVILYLLSGVPPFAETESGIFRQILQKLFDFKSDPWPTI 251
 QY 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIK 313
 DB 252 SENAKELVKQMLDRDPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIK 310
 QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGELSEIKSLMD 373
 DB 311 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGELSEIKSLMD 370
 QY 374 AADIDNSGTIDYGEFLAATLHMKNMERELVAAFSDFDKDGGVYITIDELOQACFGL 433
 DB 371 AADIDNSGTIDYGEFLAATLHMKNMERELVAAFSDFDKDGGVYITIDELOQACFGL 430
 QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMKNLNENIADAFGV 488
 DB 431 GDVHDEMKEIDQNDGRIDYAEFAAMMKGDPNMGRSRTMKNLNENIADAFGV 486

RESULT 6
 Q93XI9 PRELIMINARY; PRT; 496 AA.
 AC Q93XI9; PRELIMINARY; PRT; 496 AA.
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
 DE Calcium dependent protein kinase.
 GN RICDPK2.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee J.-Y., Yoo B.-C., Harmon A.C.; TISSUE=CELL SUSPENSION;
 RC Furuichi N., Okita T., Hara N.;
 RT "Calcium dependent protein kinase genes from resistant and susceptible
 RT potato cultivars to phytophthora infestans.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB051809; BAB63464.1; -;
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk.pkinase.
 DR InterPro; IPR002290; Ser_thr.pkinase.
 DR InterPro; IPR001245; Tyr.pkinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk.pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00219; TVTKC; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Transferase.

QY 124 EREAVKLITILGVVACHSLGVNHRDLKPNFLFDSKPKDAKAKATDFGLSVFKPGQY 183
 DB 123 EREAAKLITILGVVACHSLGVNHRDLKPNFLFDSKPKDAKAKATDFGLSVFKPGQY 182
 QY 184 LYDVVGSPPYVAPVLAACKYGPETDVMSAGVILYLLSGVPPFAETESGIFRQILQK 243
 DB 183 LYDVVGSPPYVAPVLAACKYGPETDVMSAGVILYLLSGVPPFAETESGIFRQILQ 242
 QY 244 DFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRL 303
 DB 243 DFKSDPWPTITSEGAADLIYKMLDRDPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRL 302
 QY 304 KQFSQMNKIKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGEL 363
 DB 303 KQFSQMNKIKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGEL 362
 QY 364 MESSEIKSLMDAADIDNSGTIDYGEFLAATLHMKNMERELVAAFSDFDKDGGVYITIDE 423
 DB 363 MESSEIKSLMDAADIDNSGTIDYGEFLAATLHMKNMERELVAAFSDFDKDGGVYITIDE 422
 QY 424 LQACTEGLCDTFLDDMIKEIDLNDGKIDFSEFTAMRKGDGVGRSRTMKNLNENIA 483
 DB 423 LQACTEGLCDTFLDDMIKEIDLNDGKIDFSEFTAMRKGDGVGRSRTMKNLNENIA 482
 QY 484 DAFGVGDG---EKSD 495
 DB 483 EAFGVEDTSSTAKSD 498

RESULT 5
 O24430 PRELIMINARY; PRT; 490 AA.
 AC O24430; PRELIMINARY; PRT; 490 AA.
 DT 01-JAN-1998 (TremBLrel. 05, Created)
 DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
 DE Calmodulin-like domain protein kinase isoenzyme beta.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McKendree W.L., Doostdar H., McCallum T.G., Mayer R.T.;
 RT "cDNA cloning and expression of a gene (Accession No. 297064) from
 RT Citrus paradisi roots similar to bacterial YN1 and HEA10 proteins
 RT and an mRNA from Brassica oleracea that is wound and dark inducible
 RT (PGR97-127).";
 RL Plant Physiol. 115:314-314(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lee J.-Y., Yoo B.-C., Harmon A.C.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U69173; AAB80692.1; -;
 DR HSP; P02588; 1PON.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk.pkinase.
 DR InterPro; IPR002290; Ser_thr.pkinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk.pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 490 AA; 55164 MW; 2333C41ICAA43E0F CRC64;

SQ SEQUENCE 496 AA; 55774 MW; EC41F7AED33B6DD5 CRC64;

Query Match 76.0%; Score 1969.5; DB 10; Length 496;
 Best Local Similarity 76.6%; Pred. No. 8.3e-137;
 Matches 377; Conservative 55; Mismatches 53; Indels 7; Gaps 4;

QY 1 METKP--NRRPSNTVLPYOTPRLRDHYLLGKLGQGFQGTLYLCTEKSTSANVACKSIP 58
 DB 1 MEKPATPEPKSSVWVLPYKQSLQSLYITGKLGQGFQGTTHLCLIEKSSGNLYACKTIP 60
 QY 59 KRKLVCREDYEDVWREIQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVS 118
 DB 61 KKKLICKEDYEDVWKEIQIMHLSHPNVVRIKGTYESDLYVHIVMELCAGGELFDRIVE 120
 QY 119 KGHSEAEVAVLITLGVVEACHSLGVMHRLDPENFLDPSKDDAKLKATDGLSVFY 178
 DB 121 KGHYSEREAALKIITIVGVVEACHSLGVMHRLDPENFLDPSKDDAKLKATDGLSVFY 180
 QY 179 KPGQVLYDVVGSPIYVAVPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQI 238
 DB 181 KPGETSDVGSPIYVAVPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETDGIHQI 240
 QY 239 LQKGLDFKSDPWTISEAAKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPKPLDPA 298
 DB 241 LRGKLDLSEPPWGISDSAKDLIRKLDNPKRLTAHEVLCHPWIVDTVAPDKPLDSA 300
 QY 299 VLSRLKQFSQNMKKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITTEELKAGLR 358
 DB 301 VLSRLKQFSQNMKKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITTEELKEGLR 360
 QY 359 VGSSEMESEIKSLMDAADIDNSGTIDYGEFLAATHMNMKMEREEILVAFSDFDKDGGY 418
 DB 361 VGSSEMESEIKSLMDAADIDNSGTIDYGEFLAATHMNMKMEREEILVAFSDFDKDGGY 420
 QY 419 ITIDELQACTEFGLCDPFLDDMIKEIDLNDGKIDFSEFTAMRKGDG--VGRSKTMMK 476
 DB 421 ITIELOQACKEFGSLNLDLDEIKDQDNDGQIDYGEFLAATHMNMKMEREEILVAFSDFDKDGGY 478
 QY 477 NLNFIADAFV 488
 DB 480 NL--NLGEALGL 489

RESULT 7
 Q42396 ID Q42396 PRELIMINARY; PRT; 490 AA.
 AC Q42396;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Calcium-dependent protein kinase.
 GN CDPK9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Hong Y., Takano M., Liu C.M., Gasch A., Chye M.L., Tan C.T., Koh C.C.,
 RA Chua N.H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones";
 RL DNA Res. 7:31-63(2000).

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC EMBL; U20626; AAA67657.1; -;
 DR EMBL; U20388; AAA67653.1; -;
 DR EMBL; AB025633; BAA97242.1; -;
 DR HSP; P02588; IPON;
 DR InterPro; IPR02048; EF-hand.
 DR InterPro; IPR000719; Euk.pkinase.
 DR InterPro; IPR022290; Ser_thr_kinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk.pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFR; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 490 AA; 55379 MW; 0315346396585264 CRC64;

Query Match 71.1%; Score 1844.5; DB 10; Length 490;
 Best Local Similarity 73.1%; Pred. No. 1.3e-127;
 Matches 353; Conservative 55; Mismatches 68; Indels 7; Gaps 2;

QY 1 METKPNRPSTNVLPTPRLRDHYLLGKLGQGFQGTLYLCTEKSTSANVACKSIPKR 60
 DB 1 MANKPRTR---WVLPYKTNVEDNYFLGVLGQGFQGTFLCTHKQTKGQKLACKSIPKR 56
 QY 61 KLVCREDYEDVWREIQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVSKG 120
 DB 57 KLLCEDYDDVLRQIMHLSHPNVVRIKGTYESVFEVHIVMEVCEGELFDRLVSKG 116
 QY 121 HFSREAVKLIITLGVVEACHSLGVMHRLDPENFLDPSKDDAKLKATDGLSVFYKP 180
 DB 117 HYSEREAALKIITIVGVVEACHSLGVMHRLDPENFLDPSKDDAKLKATDGLSVFYKP 176
 QY 181 GOYLDVVGSPYVAVPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQ 240
 DB 177 GEAFSELVGSAYVAVPEVLKHYGPECDVWSAGVILYILLSGVPPFWAETESGIFRQILQ 236
 QY 241 GKLDKSDPWTISEAAKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPKPLDPAVL 300
 DB 237 GKLEFEINPWPSSISAKDLIKKMLERNPKRLTAHQVLCHEPWIVDDKVPDKPLDCAV 296
 QY 301 SRLKQFSQNMKKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITTEELKAGLRV 360
 DB 297 SRLKQFSQNMKKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITTEELKAGLRV 356
 QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATHMNMKMEREEILVAFSDFDKDGGYIT 420
 DB 357 SELMESEIKSLMDAADIDNSGTIDYGEFLAATHMNMKMEREEILVAFSDFDKDGGYIT 416
 QY 421 IDELOQACTEFGLCDPFLDDMIKEIDLNDGKIDFSEFTAMRKGDGVR---RTMMKN 477
 DB 417 IEELQACKEFGSLNLDLDEIKDQDNDGQIDYGEFLAATHMNMKMEREEILVAFSDFDKDGGYIT 476
 QY 478 LNF 480
 DB 477 LNF 479

RESULT 8
 Q9FXQ3 ID Q9FXQ3 PRELIMINARY; PRT; 551 AA.
 AC Q9FXQ3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE OSCDPK7.
 GN OSCDPK7.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONARE;
RX MEDLINE=20387027; PubMed=10929125;
RA Saijo Y., Hata S., Kiyozuka J., Shimamoto K., Izui K.;
RT "Over-expression of a single Ca²⁺-dependent protein kinase confers
RT both cold and salt/drought tolerance on rice plants.";
RL Plant J. 23:319-327(2000).
DR EMBL; AB042550; BAB1688.1; -.
DR HSSP; P02593; 1CTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW ATP-binding; Transferase.
SQ SEQUENCE 551 AA; 60966 MW; B479A089EF287A7B CRC64;

Query Match 68.4%; Score 1773; DB 10; Length 551;
Best Local Similarity 71.2%; Pred. No. 2.9e-122;
Matches 339; Conservative 53; Mismatches 82; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGQGGFTYLCCTEKSTSNYACKSIPKRLKVCREDYEDVW 72
DB 75 SVLGHTPTNLRDLVAMGRKLGQGGFTYLCCTELSTGVYACKSISKRKLITKEDVDVR 134
QY 73 REIQIMHLSHPNVRIKGTYESVFVHYVMEYCEGELFDRIVSGHSEAEVAVKLK 132
DB 135 REIQIMHLSGHKNVVAIKGAYEDQVYVHYVMEYCEGELFDRIVSGHSEAEVAVKLK 194
QY 133 TILGVVACHSLGVHMDLKPENFLFSPKDDAKLKATDFGLSVFYKPGQYLDVVGSPY 192
DB 195 IIVGVVACHSLGVHMDLKPENFLFSPKDDAKLKATDFGLSVFYKPGQYLDVVGSPY 254
QY 193 YVAPEVLKKGYPETDVMWAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPWP 252
DB 255 YVAPEVLKKGYPETDVMWAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPWP 314
QY 253 ISEAKDLIYKMLERSPKRISAEALCHPWIVDEQAPDKPLDPVAVLSRLKQFSQNMKI 312
DB 315 ISEAKDLIYKMLERSPKRISAEALCHPWIVDEQAPDKPLDPVAVLSRLKQFSQNMKI 374
QY 313 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGITTFEELKAGLRKRVGSELMESEIKSLM 372
DB 375 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGITTFEELKAGLRKRVGSELMESEIKSLM 434
QY 373 DAADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYITIDELQSNCTEFG 432
DB 435 DAADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYITIDELQSNCTEFG 494
QY 433 LCDTDLDMKIEIDNDGKIDFSEFTAMRRKGD-GVGRSTTMMKNLNFNIADAFG 487
DB 495 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMRNSLNIISMRDAPG 549

RESULT 9

O04417

ID O04417 PRELIMINARY; PRT; 492 AA.

AC O04417;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcium dependent protein kinase.
GN ZMCDPK1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTUM;
RA Berberich T., Kusano T.;
RT "Cycloheximide induces a subset of low-temperature-inducible genes in
RL maize.";
RL Mol. Gen. Genet. 0:0-0(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTUM;
RX MEDLINE=97294505; PubMed=9150261;
RA Berberich T., Kusano T.;
RT "Cycloheximide induces a subset of low temperature-inducible genes in
RT maize.";
RL Mol. Gen. Genet. 254:275-283(1997).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D84408; BAA12338.1; -.
DR HSSP; P02593; 1CTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 492 AA; 54734 MW; 8615C3C360CE949 CRC64;

Query Match 67.6%; Score 1752; DB 10; Length 492;
Best Local Similarity 70.6%; Pred. No. 8.7e-121;
Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGQGGFTYLCCTEKSTSNYACKSIPKRLKVCREDYEDVW 72
DB 14 SVLGHTPTNLRDLVAMGRKLGQGGFTYLCCTELATIDYACKSISKRKLITKEDVDVR 73
QY 73 REIQIMHLSHPNVRIKGTYESVFVHYVMEYCEGELFDRIVSGHSEAEVAVKLK 132
DB 74 REIQIMHLSGHKNVVAIKGAYEDQVYVHYVMEYCEGELFDRIVSGHSEAEVAVKLK 133
QY 133 TILGVVACHSLGVHMDLKPENFLFSPKDDAKLKATDFGLSVFYKPGQYLDVVGSPY 192
DB 134 IIVGVVACHSLGVHMDLKPENFLFSPKDDAKLKATDFGLSVFYKPGQYLDVVGSPY 193
QY 193 YVAPEVLKKGYPETDVMWAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPWP 252
DB 194 YVAPEVLKKGYPETDVMWAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPWP 253
QY 253 ISEAKDLIYKMLERSPKRISAEALCHPWIVDEQAPDKPLDPVAVLSRLKQFSQNMKI 312
DB 254 ISEAKDLIYKMLERSPKRISAEALCHPWIVDEQAPDKPLDPVAVLSRLKQFSQNMKI 313
QY 313 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGITTFEELKAGLRKRVGSELMESEIKSLM 372
DB 314 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGITTFEELKAGLRKRVGSELMESEIKSLM 373
QY 373 DAADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYITIDELQSNCTEFG 432

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QY 433 LCTPTLDDMKELDLNDCKIDSEFTAMMRKGD-GVGRSRTMKMLNFNFIAD 484
Db 434 MPDAFLDDVINADQNDGRIDYGEFVAMTKGMVGR-RTMRNSLNISMRD 485

RESULT 10
Q43676 PRELIMINARY; PRT; 487 AA.
ID Q43676
AC Q43676;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium dependent protein kinase.
GN CDPK.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RWILCZ, AND CV. BERKEN; TISSUE=ETIOLATED HYPOCOTYL;
RX MEDLINE=96311003; PubMed=8704124;
RA Botella J.R., Arteca J.M., Somodevilla M., Arteca R.N.;
RT "Calcium-dependent protein kinase gene expression in response to
RT physical and chemical stimuli in mungbean (Vigna radiata).";
RL Plant Mol. Biol. 30:1129-1137(1996).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U08140; AAC49405.1; -
DR HSSP: Q63450; 1A06.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00036; ehand; 4.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; EFh; 4.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 487 AA; 54700 MW; 54E6PF5D93AEB2C CRC64;

Query Match 67.1%; Score 1751; DB 10; Length 487;
Best Local Similarity 70.0%; Pred. No. 1e-120;
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;

QY 14 VLPYOTPLRDHYLLGKLGQSGFTTYLCTEKSTSANYSACKSIPKRLVCREYEDVWR 73
Db 12 VLGHKTPNRLDYTLGRKLGQSGFTTYLCTENSTNYSACKSISKRRLSKEDVEDVR 71

QY 74 EIQIMHHLSEHPNVRIKGTEDSVFVHIVMEVCEGGELFDRIYVSKGFSEAEVAKLIK 133
Db 72 EIQIMHLAGKNIVTIKAYEDPLVYHIVMELCSGELFDRIQGHYTERKAAELTKI 131

QY 134 ILGVVEACHSLGMVHRDLKPNFLFDSPKDAKLKATDFGLSVFYKPGQYLVDVVGSPY 193
Db 132 IVGVVEACHSLGMVHRDLKPNFLVKNDDDFSLKAIDFGLSVFYKPGQITDVGSPY 191

QY 194 VAPVLYKCYGPEIDVWSAGVILYLLSGVPPFWAETESCFRQILQGLDKFSDPWPTI 253
Db 192 VAPVLYKCYGPEADVWTAGVILYLLSGVPPFWAETQQGIFDAVLKGVHIDFSDPWPLI 251

QY 254 SEAAKDLIVKMLERSPKKRISAEALCHPWIVDEQAAPKPLDPAVLSRLKQFSOMNKIK 313
Db 252 SDGKDLIRKMLCSQSERIATQVLCHPWICENGAVPADRAIDPAVLSRLKQFSAMNKLK 311

QY 314 KMALRVIAERLSSEIEGLKELFKMIDTNSGTITFEELKAGLRVGSSELMESEIKSLMD 373

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QY 374 AADIDNSGTIDYIEFTAAATLHNLKLEREBHLVAAPSYFDKDGSGYITVDELQACKHN 433
Db 372 AADVKSIGTIIDYIEFTAAATVHLNKLREBHLIAAFQVFDKDGSGYITVDELQACKHN 431
QY 434 COTPLDDMIKEIDLNDGKIDSEFTAMMRKGD-GVGRSRTMKMLNFNFIAD 485
Db 432 TDAFLIEDIREDQNDGRIDYGEFVAMTKGMVGR-RTMRNSLNISMRD 483

RESULT 11
O04123 PRELIMINARY; PRT; 554 AA.
ID O04123
AC O04123;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium-dependent protein kinase.
GN Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INBRED LINE H84;
RX MEDLINE=97201047; PubMed=9048876;
RA Saijo Y., Hata S., Sheen J., Izui K.;
RT "cDNA cloning and prokaryotic expression of a maize calcium-dependent
RT protein kinase.";
RL Biochim. Biophys. Acta 1350:109-114(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D87042; BAA13232.1; -
DR HSSP: P02593; 1CTR.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00036; ehand; 4.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; EFh; 4.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 554 AA; 61056 MW; 51FC6F44684C57C6 CRC64;

Query Match 67.3%; Score 1745; DB 10; Length 554;
Best Local Similarity 70.0%; Pred. No. 3.4e-120;
Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;

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Db 78 SVLGHKTPNRLDYTLGRKLGQSGFTTYLCTENSTNYSACKSISKRRLSKEDVEDVR 137

QY 73 EIQIMHHLSEHPNVRIKGTEDSVFVHIVMEVCEGGELFDRIYVSKGFSEAEVAKLIK 132
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QY 133 ILGVVEACHSLGMVHRDLKPNFLFDSPKDAKLKATDFGLSVFYKPGQYLVDVVGSPY 192
Db 198 ILGVVEACHSLGMVHRDLKPNFLVKNDDDFSLKAIDFGLSVFYKPGQITDVGSPY 257

QY 193 YVAPVLYKCYGPEIDVWSAGVILYLLSGVPPFWAETESCFRQILQGLDKFSDPWPT 252
Db 258 YVAPVLYKCYGPEADVWTAGVILYLLSGVPPFWAETQQGIFDAVLKGVHIDFSDPWPT 317

QY 253 ISPAKDLIVKMLERSPKKRISAEALCHPWIVDEQAAPKPLDPAVLSRLKQFSOMNKI 312

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DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR	PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS0108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW	ATP-binding; Kinase; Transferase.
SQ	SEQUENCE 578 AA; 64723 MW; 88778B73F85A16B6 CRC64;

Query Match	66.9%; Score 1733.5; DB 10; Length 578;
Best Local Similarity	67.4%; Pred.No. 2.6e-119;
Matches 325; Conservative	62; Mismatches 80; Indels 15; Gaps
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QY	2	ETKENPRRP-----SNTVLFPQTPLRDLHYLLGKGLGGQGFGTITLCTEK	46
DB	75	EKEEQKKPKPAEMKRVSAGLTSDVLOKTKNLEFFSIGKGLGGQGFTFKCKVEK	134
		: :	
QY	47	STSNYACKSPKRLVKREDYEDWRBEIQIMHLSBPNVVRIRKGTYESVFVIHYMEV	106
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DB	135	ATGREYACKSAKRKLTLTDDEVDVRRREVQIMHHLAGHPHVISIKGAYEDAVAVHVNMF	194
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QY	107	CEGELEDRIYSKGHFSSEREAVKLIKTILGVVEACHSLGVMHRLDKPENFLFDSPKDOK	166
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DB	195	CAGGELDRIIQRGHYTERKAELTRIVGVVEACHSLGVMHRLDKPENFLFDQKEDSL	254
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QY	167	LKATDFGLSVFYKPGQVLYLVVGSPYYVAPVELVKCCYGPETIDVMSAGVILIYLLSGVPFF	226
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DB	255	LKATDFGLSIIFKPGDRPTDVGGSPYYVAPVELVKRYGFEADVMSAGVIIYILLSGVPFF	314
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QY	227	WAETESGFRTIOLOGKLDKFSDPPTTISEAKDLITYKMLESPPKRIISAHEALCHPWIVD	286
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DB	315	WAENEQGIIEGVHLGGDLDTSDPWPISIEDAKDLMMRLVMDPRRLTAHEVLCHPWVQV	374
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QY	287	BQAAPDKPLDPAPVLSRLUKQFSQMKNKKMVALRIAERLSEEEIGLKLFKMTDTSNGT	346
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DB	375	DGVAPDKPLDSAVLSRMKQFSAMNKLMKVALRIAELSSEEEIAGLKMKFMKMTDTSNGQ	434
	:	: : : : ~~~~~~ :	
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DB	495	AFCYFDKDGSGYITADELQQACEEGIGDVRWEEMIREAQDNQDGRIDYNEFVAMMQGN	554
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DB	555	PV 556	

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ID Q38872	
AC Q38872;	
DT 01-NOV-1996 (TREMBLrel. 01, Created)	
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Calmodulin-domain protein kinase CDPK isoform 6.	
GN CPK6 OR F5J6.5.	
OS Arabidopsis thaliana (Mouse-ear cress).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.	
OX NCBI_taxid=3702;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=COLUMBIA;	
RA Hrabak E.M., Dickmann I.J., Satterlee J.S., Sussman M.R.;	
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.	
RN [2]	
RP SEQUENCE FROM N.A.	
RC STRAIN=CV. COLUMBIA;	
RA Zhong J.-M., Ma P.N., Parnell L.D., Chen C.-N., Chen E.Y.;	
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.	
RN [3]	
RP SEQUENCE FROM N.A.	

Mon Mar 31 13:53:38 2003

RC STRAIN-CV. COLUMBIA;
RA Parnell L., McCombie W.R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
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RC STRAIN-CV. COLUMBIA;
RA Zhong J.M., Ma P.N., Parnell L.D., Chen C.-N., Chen E.Y.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
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RA STRAIN-CV. COLUMBIA;
RL Parnell L.;
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RC -; SIMILARITY (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -; SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC EMBL; U31835; AAB03246.1; -;
DR EMBL; AC002329; AAB86506.1; -;
DR HSP; P02593; 1CTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Eph; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR AP- binding: Serine/threonine-protein kinase: Transferase.
SW K0
SQ SEQUENCE 544 AA: 61111 MW: 6A4F047BEE95E4F CRC64;

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 08:35:21 ; Search time 5487 Seconds
(without alignments)
9266.011 Million cell updates/sec

Title: US-09-848-806-2
Perfect score: 1747
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Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 6: gb_pat.*
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- 10: gb_ro.*
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- 13: gb_un.*
- 14: gb_vi.*
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- 16: em_fun.*
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- 38: em_sy.*
- 39: em_hngo_hum.*
- 40: em_hngo_mus.*
- 41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1515.8	86.8	1519	8	AY113986	AY113986 Arabidops
4	1202.4	68.8	1657	8	ATU31752	U31752 Arabidopsis
5	826.4	47.3	1754	8	GMU69173	U69173 Glycine max
6	803.6	46.0	1732	8	AB051809	AB051809 Solanum t
7	756.4	43.3	1768	8	AX077706	AX077706 Sequence
8	756.4	43.3	1768	8	SOXCADPK	M64987 Glycine max
9	744.2	42.6	1693	8	ATACDPK9	U20388 Arabidopsis
10	712.6	40.8	2036	8	ATU31835	U31835 Arabidopsis
11	706.2	40.4	1858	8	ATHATCDPK	D28582 Arabidopsis
12	698.4	40.0	2393	8	AB051808	AB051808 Solanum t
13	696.8	39.9	2437	8	NTA344155	AJ344155 Nicotiana
14	688.4	39.4	1967	8	ATU31834	U31834 Arabidopsis
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16	666	38.1	2019	8	NTA344154	AY072801 Cucurbita
17	657.6	37.6	2270	8	AY072801	AX077715 Sequence
18	652.6	37.4	2550	6	AX077715	U90262 Cucurbita p
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20	652.2	37.3	1746	8	NBE344156	AB042550 Oryza sat
21	649.4	37.2	2126	8	AB042550	AY072802 Cucurbita
22	649	37.1	2214	8	AY072802	L14771 Arabidopsis
23	645	36.9	2214	8	ATHCALLIPR	D84408 Maize mRNA
24	643.4	36.8	1857	8	D84408	U31833 Arabidopsis
25	641.8	36.7	2142	8	ATU31833	AX077717 Sequence
26	629.8	36.1	2022	6	AX077717	U08140 Vigna radia
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30	596.2	34.1	1041	8	AY030280	AX077709 Sequence
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ALIGNMENTS

RESULT 1
ATHCDPKB
LOCUS
DEFINITION Arabidopsis thaliana mRNA for calcium-dependent protein kinase
(CDPK), complete cds.
1747 bp mRNA linear PLN 05-FEB-1999
ACCESSION D21806
VERSION D21806.1 GI:1235717
KEYWORDS calcium-dependent protein kinase; ATCDPK2.
SOURCE Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1747)
AUTHORS Urao,T., Katagiri,T., Mizoguchi,T., Yamaguchi-Shinozaki,K.,

Hayashida, N. and Shinozaki, K.
Two genes that encode Ca(2+)-dependent protein kinases are induced
by drought and high-salt stresses in Arabidopsis thaliana
Mol. Gen. Genet. 244 (4), 331-340 (1994)
94359455
2 (bases 1 to 1747)
Shinozaki, K.
Direct Submission
Submitted (30-OCT-1993) Kazuo Shinozaki, Tsukuba Life Science
Center, The Inst. of Physical and Chemical Res.; 3-1-1 Kohyadai,
Tsukuba, Ibaraki 350, Japan (E-mail: sinozaki@erts1.riken.go.jp,
Tel: 0298-36-4359, Fax: 0298-36-9060)
On Mar 22, 1996 this sequence version replaced gi:540482.

COMMENT

Location/Qualifiers

FEATURES

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/strain="Columbia"

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67..1554

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/evidence=experimental

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/db_xref="GI:604881"

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primer_bind

order(500..531, complement(1301..1323))

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polya_site

1747

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BASE COUNT

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RESULT 3
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LOCUS Arabidopsis thaliana putative calcium-dependent protein kinase
DEFINITION (At1g35670) mRNA, complete cds.
ACCESSION AY113986
VERSION AY113986.1 GI:21281140
KEYWORDS FLI-CDNA.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rhamniophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1519)
AUTHORS Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C.J., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
2 (bases 1 to 1519)
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C.J., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA : RIKEN
Arabidopsis Full-length cDNA): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
Hayashizaki,Y. and Shinozaki,K.
The Salk, Stanford, PGECC (SSP) Consortium members constructed and
sequenced the pUN1 (ORF) clones using the RAPL cDNAs: Yamada,K.,
Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,
Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
Davis,R.W., Ecker,J.R. and theologis,A.
Yamada,K. (SSP/PGECC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
/PGECC) contributed equally to this work as PIs.
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Location/Qualifiers
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1489..1519

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BASE COUNT 448 a 279 c 366 g 426 t

ORIGIN

Query Match

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Matches 1517; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4

ATU31752

LOCUS

DEFINITION

Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform

4 (CPK4) mRNA, partial cds.

ACCESSION

U31752

ATU31752 1657 bp mRNA linear PLN 23-AUG-2001
 Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform
 4 (CPK4) mRNA, partial cds.


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RESULT 6
AB051809
LOCUS
DEFINITION Solanum tuberosum RiCDPK2 mRNA for calcium dependent protein
AB051809
ACCESSION AB051809
VERSION AB051809.1 GI:15289759
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (cultivar:Rishiri) cell suspension cDNA to mRNA,
clone_lib:potato cv. Rishiri cDNA.
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
1
Furuichi,N., Okuta,T. and Hara,N.
Calcium dependent protein kinase genes from resistant and
susceptible potato cultivars to Phytophthora infestans
Unpublished
2 (bases 1 to 1732)
Furuichi,N. and Okuta,T.
Direct Submission
Submitted (25-NOV-2000) Naotaka Furuichi, Niigata university,
Agriculture; 2-8050, Igarashi, Niigata shi, Niigata ken 950-2181,
Japan (E-mail:nfuru@agr.niigata-u.ac.jp, Tel:81-25-262-7520(ex.7520),
URL:http://www.niigata-u.ac.jp, Tel:81-25-262-7520),
Fax:81-25-262-7520)
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Matches 1080; Conservative 0; Mismatches 419; Indels 5; Gaps 2;

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<div> <div>SOYCADPK</div> <div>Glycine max calcium dependent protein kinase mRNA.</div> <div>M64987.1</div> <div>GI:169930</div> <div>calcium/calmodulin-dependent protein kinase.</div> <div>Glycine max cDNA to mRNA.</div> <div>Glycine max</div> <div>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.</div> <div>1 (bases 1 to 1768)</div> <div>Harper, J.F., Sussman, M.R., Schaller, G.E., Putnam-Evans, C., Charbonneau, H. and Harmon, A.C.</div> <div>A calcium-dependent protein kinase with a regulatory domain similar to calmodulin</div> <div>Science 252 (5008), 951-954 (1991)</div> <div>91240279</div> <div>1852075</div> </div>			
<div> <div>REFERENCE</div> <div>AUTHORS</div> <div>TITLE</div> <div>JOURNAL</div> <div>MEDLINE</div> <div>PUBMED</div> <div>FEATURES</div> <div>source</div> </div>			
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RESULT 9
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LOCUS
DEFINITION Arabidopsis thaliana calcium dependent protein kinase mRNA, complete cds.
ACCESSION U20388
VERSION 020388.1
KEYWORDS GR:836937
SOURCE calcium dependent protein kinase.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1693)
Hong,Y., Takano,M., Liu,C.M., Gasch,A., Chye,M.L. and Chua,N.H.
Expression of three members of the calcium-dependent protein kinase gene family in Arabidopsis thaliana
Plant Mol. Biol. 30 (6), 1259-1275 (1996)
96311013
8704134
FBIED
JOURNAL
MEDLINE
REFERENCE
AUTHORS Hong,Y.
TITLE Direct Submission
SUBMITTED (27-JAN-1995) Yan Hong, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore, Republic of Singapore, 0511
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1693

polya_site

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RESULT 10
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DEFINITION Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 6 (CPK6) mRNA, complete cds.
ACCESSION U31835
VERSION U31835.1
KEYWORDS GI:1399274
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 2036)
Hrabak,E.M., Dickmann,L.J., Satterlee,J.S. and Sussman,M.R.
Characterization of eight new members of the calmodulin-like domain
protein kinase gene family from Arabidopsis thaliana
Plant Mol. Biol. 31 (2), 405-412 (1996)
96343943
MEDLINE 8756605
PUBMED 8756605
REFERENCE 2 (bases 1 to 2036)
AUTHORS Hrabak,E.M.
DIRECT SUBMISSION
TITLE Submitted (18-JUL-1995) Estelle Hrabak, Horticulture, University of
Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
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On Mar 10, 1996 this sequence version replaced gi:535778.

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DEFINITION	(cdpk3 gene).		
ACCESSION	AJ344155		
VERSION	AJ344155.1	GI:16215470	
KEYWORDS	calcium-dependent protein kinase; cdpk3 gene.		
SOURCE	common tobacco.		
ORGANISM	Nicotiana tabacum		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.			
REFERENCE 1	Romeis,T., Ludwig,A.A., Martin,R. and Jones,J.D.		
AUTHORS	Calcium-dependent protein kinases play an essential role in a plant		
TITLE	defence response		
JOURNAL	EMBO J. 20 (20), 5556-5567 (2001)		
MEDLINE	21481752		
PUBMED	11597999		
REFERENCE 2	(bases 1 to 2437)		
AUTHORS	Romeis,T.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-AUG-2001) Romeis T., The Sainsbury Laboratory, John		
	Innes Centre, Norwich, Colney Lane, Norfolk, NR4 7UH, UNITED		
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Best Local Similarity	65.1%	Pred. No. 2.6e-140;	
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RESULT 14
ATU31834
LOCUS
DEFINITION
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5 (CPK5) mRNA, complete cds.
ACCESSION
U31834
VERSION
U31834.1 GI:1399272
KEYWORDS
Arabidopsis thaliana.
SOURCE
Arabidopsis thaliana
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1967)
Hrabak,E.M., Dickmann,L.J., Satterlee,J.S. and Sussman,M.R.
Characterization of eight new members of the calmodulin-like domain
protein kinase gene family from Arabidopsis thaliana
Plant Mol. Biol. 31 (2), 405-412 (1996)
96343943
PUBMED
8756605
2 (bases 1 to 1967)
Hrabak,E.M.
Direct Submission
Submitted (18-JUL-1995) Estelle Hrabak, Horticulture, University of
Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
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VERSION	AC007887.9
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SOURCE	Arabidopsis thaliana
ORGANISM	Arabidopsis thaliana
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Ecker, J.R.
 Submitted (22-JUN-1999)
 Department of Biology, University of Pennsylvania, 38th Street and
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
 2 (bases 1 to 158096)

REFERENCE	2 (bases 1 to 158096)
AUTHORS	Ecker, J.R.
TITLE	Direct Submission
JOURNAL	Submitted (04-OCT-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
REFERENCE	3 (bases 1 to 158096)

REFERENCE
AUTHORS

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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29	444.4	25.4	2087	22	AAF74286	Arabidopsis calciu
30	405.8	23.2	1133	22	AAQ58333	Tobacco homolog of
31	379.8	21.7	921	20	AAC522757	Tobacco CDPK cDNA.
32	346.2	19.8	1020	19	AAV36878	Nucleotide sequenc
33	346.2	19.8	1020	22	AAI66819	ATCDEPK1A PK domain
34	337.6	19.3	1412	21	AAC51681	Zea mays DNA fragm
35	326	18.7	956	22	AAF74289	Peanut calcium dep
36	299	17.1	1781	21	AAQ34898	Arabidopsis thalia
37	290.6	16.6	1798	24	ABK71570	Human dithp polynu
38	277.8	15.9	1387	24	ABA91068	Physcomitrella pat
39	227.4	13.7	2210	22	AAF74279	Potato calcium dep
40	227.4	13.0	955	24	ABN98558	Arabidopsis thalia
41	221.6	12.7	2254	24	ABA91080	Physcomitrella pat
42	220.6	12.6	1785	21	AAC51470	Arabidopsis thalia
43	204.6	11.7	2202	21	AAQ37415	Arabidopsis thalia
44	189.6	10.9	2374	22	AAH46998	Rice CDPK cDNA (cl
45	183.2	10.5	13114	21	AAA60744	Rice gene for resi

ALIGNMENTS

RESULT 1	
ABA06021	
ID ABA06021 standard; cDNA; 1747 BP.	
XX AC	
ABA06021;	
XX AC	
08-MAR-2002 (first entry)	
XX DT	
XX DE	
Arabidopsis CDPK2 encoding polynucleotide SEQ ID NO 2.	
XX KW	
Arabidopsis; CDPK2; CDPK4; calcium dependent protein k	
KW KW	
disease resistance; agricultural; pathogen; crop yield	
KW KW	
fungicide; bactericide; nematocide; insecticide; viric	
transgenic; plant; enzyme; gene; ss.	
XX XX	
OS OS	
Arabidopsis thaliana.	
XX PH	
Key Location/Qualifiers	
CDS 67..1554	
FT FT	/tag= a
FT FT	/product= "CDPK2"
XX WC200184911-A1.	
PN PN	
15-NOV-2001.	
XX PD	
XX PP	
04-MAY-2001; 2001WO-US14368.	
XX PR	
05-MAY-2000; 2000US-201925P.	
XX PA	
(GCHO) GEN HOSPITAL CORP.	
XX XX	

PI XX Sheen J;
DR DR WPI; 2002-062179/08.
XX P-PSDB; AAM48000.

PT Producing plant having increased disease resistance, comprises
PT regenerating plant from a non-naturally occurring plant cell
PT over-expressing a polynucleotide encoding a calcium dependent protein
XX kinase polypeptide -
XX
XX Disclosure; Fig 1; 44pp; English.

CC The invention relates to producing a plant having increased disease
CC resistance, comprising providing a non-naturally occurring plant cell
CC over-expressing a polynucleotide encoding a calcium dependent protein
CC kinase (CDPK) polypeptide and regenerating a plant from the plant
CC cell, where the CDPK polypeptide is expressed in the plant, increasing
CC the resistance of the plant to disease as compared to a
CC naturally-occurring plant. The method is useful for a variety of
CC agricultural and commercial purposes including improving a plant's
CC resistance against plant pathogens, increasing crop yields, improving
CC crop and ornamental quality and reducing agricultural production costs.
CC The method facilitates an effective and economical method for in-plant
CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g., application of fungicides,
CC bactericides, nematocides, insecticides, or viricides) that are typically
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Abradidopsis
CC thaliana CDPK2 of the invention.

XX
SQ Sequence 1747 BP; 516 A; 316 C; 392 G; 523 T; 0 other;

Query Match 100.0%; Score 1747; DB 24; Length 1747;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GATCCGGGTACATATTCTTCTTCCTTTCAAAATCGAGATCGAAGAAGAACCAACAATAAAA	60
Db	1	GATCCGGGTACATATTCTTCTTCTTCTTCAANTCGAGATCGAAGAAGAACCAACAATAAAA	60
QY	61	CCAAAAATGAGACGAAGCACCACCCCTAGACGTCCTTCAAACACAGTGTTCTACCATATCAA	120
Db	61	CCAAAAATGAGACGAAGCACCACCCCTAGACGTCCTTCAAACACAGTGTTCTACCATATCAA	120
QY	121	ACACCAGGATTAAAGAGATCATTAACCTTCTGGGAAAAAGCTAGGCCAGGCCAATTGGA	180
Db	121	ACACCAGGATTAAAGAGATCATTAACCTTCTGGGAAAAAGCTAGGCCAGGCCAATTGGA	180
QY	181	ACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTACGCGCTGCAAAATCGATCCG	240
Db	181	ACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTACGCGCTGCAAAATCGATCCG	240
QY	241	AAGCGAAGCTCGTGTGCGGAGGATTACGAAGATGATGCGGTGAGATTCAGATCATG	300
Db	241	AAGCGAAGCTCGTGTGCGGAGGATTACGAAGATGATGCGGTGAGATTCAGATCATG	300
QY	301	CATCATCTCTGAGCATCCAATGTTGTAGGATCAAAAGGACTTATGAAGATTCGGTG	360
Db	301	CATCATCTCTGAGCATCCAATGTTGTAGGATCAAAAGGACTTATGAAGATTCGGTG	360
QY	361	TTGTTTCATATGTTATGAGGTTTGTCAAGGTCGTGAGCTTTTTGATCGGATTTCT	420
Db	361	TTGTTTCATATGTTATGAGGTTTGTGAAGTGTGCTGAGCTTTTGTATCGGATTTCT	420
QY	421	AAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTTCTGGTGTGTT	480
SQ		AA	

Db	421	AAAGGTCATTTTAGTGAGCGGTGCAAGCTGTCAAGCTTATTAAAGACGATTTCTTGGTGTGTT	480
QY	481	GAGGCTTGTTCATTTCTTGGTGTATTGATAGAGATCTCAAAACCTCAGAAATTTCTTGT	540
Db	481	GAGGCTTGTTCATTTCTTGGTGTATTGATAGAGATCTCAAAACCTCAGAAATTTCTTGT	540
QY	541	GATAGTCTCTAAAGATGATGCTTAAGCTTAAGGCTAACGATTTTGGTGTGCTGCTTCTAT	600
Db	541	GATAGTCTCTAAAGATGATGCTTAAGCTTAAGGCTAACGATTTTGGTGTGCTGCTTCTAT	600
QY	601	RAGCCAGGACAAATATTATATGACGTAGTTGGAAGTCCGCTACTATGTTCCACACAGAGTG	660
Db	601	RAGCCAGGACAAATATTATATGACGTAGTTGGAAGTCCGCTACTATGTTCCACACAGAGTG	660
QY	661	CTAAGAAATGTTATGGACCTGAAATAGATGTGTGAGTGTGGTGTGTTTCTCTACAT	720
Db	661	CTAAGAAATGTTATGGACCTGAAATAGATGTGTGAGTGTGGTGTGTTTCTCTACAT	720
QY	721	TTACTCAGCGGTGTCCTCCCTTCGGGCAGAGACTGAGTCTGGATCTTTTACAGAGATA	780
Db	721	TTACTCAGCGGTGTCCTCCCTTCGGGCAGAGACTGAGTCTGGATCTTTTACAGAGATA	780
QY	781	TGCAAGGGAAGTTAGATTTCAAAATCTGACCGTGGCTTACTATCTCAGAAGCTGCTAAA	840
Db	781	TGCAAGGGAAGTTAGATTTCAAAATCTGACCGTGGCTTACTATCTCAGAAGCTGCTAAA	840
QY	841	GATTTGATCTATAAAATGCTCAAAAGGAGCCCCCAAGAACGATTTCTCTCATGAAGCC	900
Db	841	GATTTGATCTATAAAATGCTCAAAAGGAGCCCCCAAGAACGATTTCTCTCATGAAGCC	900
QY	901	TTGCTCACCCATGGATTGTCGATGAACAAGCAGCACCAGACAAGCCTTTGATCCAGCA	960
Db	901	TTGCTCACCCATGGATTGTCGATGAACAAGCAGCACCAGACAAGCCTTTGATCCAGCA	960
QY	961	GTCCTTATCTGCTTAAAGCAGTTTTCTCAAAATGATTAAGATTTAAGAAATGSCATACGG	1020
Db	961	GTCCTTATCTGCTTAAAGCAGTTTTCTCAAAATGATTAAGATTTAAGAAATGSCATACGG	1020
QY	1021	GTAATTTGCTGAGAGACTTTTCAGAGGAAGAAATTTGGAGGTCTTGAAGGAATTTGTCAGATG	1080
Db	1021	GTAATTTGCTGAGAGACTTTTCAGAGGAAGAAATTTGGAGGTCTTGAAGGAATTTGTCAGATG	1080
QY	1081	ATAGACACAGACAACAGCGGACGATTACTTTTGAAGACTCAAAGCGGTTTGAAGAGA	1140
Db	1081	ATAGACACAGACAACAGCGGACGATTACTTTTGAAGACTCAAAGCGGTTTGAAGAGA	1140
QY	1141	GTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCTCATGTCGCGCTGATATCGAC	1200
Db	1141	GTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCTCATGTCGCGCTGATATCGAC	1200
QY	1201	AACAGTGTGTAATAGACTACGGAGATTCCTAGCAGCAACCTTACATGTAACAAAGATG	1260
Db	1201	AACAGTGTGTAATAGACTACGGAGATTCCTAGCAGCAACCTTACATGTAACAAAGATG	1260
QY	1261	GAGAGAGAGGAGATTTCTGCTGCTGCAATTTTCGGACTTTGACAAAGACGGAACGGTTAT	1320
Db	1261	GAGAGAGAGGAGATTTCTGCTGCTGCAATTTTCGGACTTTGACAAAGACGGAACGGTTAT	1320
QY	1321	ATCACCATCGATGAGCTTACGTACAGAGTTGACAGAGTTTGGTGTATGATACACCTCTG	1380
Db	1321	ATCACCATCGATGAGCTTACGTACAGAGTTTGGTGTATGATGATACACACCTCTG	1380
QY	1381	GACGACATGATCAAGGAGATTGATCTTCACATGACGGGAAGATCGATTTCTCGAGTTT	1440
Db	1381	GACGACATGATCAAGGAGATTGATCTTCACATGACGGGAAGATCGATTTCTCGAGTTT	1440
QY	1441	ACAGCAATGATCAGSAAAGGAGATGGAGTTGGGAGAACGACAACCATGATCAAGAACTTG	1500
Db	1441	ACAGCAATGATCAGSAAAGGAGATGGAGTTGGGAGAACGACAACCATGATCAAGAACTTG	1500
QY	1501	AACCTCAACATTTGCTGATGCTTTTGGAGTTGATGGTGAATAATCTGATGACTCATC	1560
Db	1501	AACCTCAACATTTGCTGATGCTTTTGGAGTTGATGGTGAATAATCTGATGACTCATC	1560


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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
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PR 02-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.7%; Score 1183.2; DB 21; Length 1506;
Best Local Similarity 88.2%; Pred. No. 3.5e-258;
Matches 1287; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 75 GAAGCCAAACCCCTAGACGTCCTTCAACACAGTTCACCATATCAACACACGAGTAAAG 134
DB 6 GAAACCAACCCCTAGAACCCCTCAACACAGTGTCTTCCATAGAACACCAAGATTAAG 65
QY 135 AGATCATTACCTTCTGGGAAAAAGCTAGGCCAAGCCCAATTTGGAAACACCTATCTCTG 194
DB 66 AGATCATTATCTCTCGGCAAAAGCTAGGCCAAGCCCAATTTGGAAACACCTATCTCTG 125
QY 195 CACAGAGAAATCAACCTCCGCTAATTAACGCTCAATCGATCCGCAAGCGAAAGCTCT 254
DB 126 TACAGAGAAATCATCATCAGTAAATTAACGCTTGAATCAATCCCAAAACGTAAGCTTCT 185
QY 255 GTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATTCAGATCATCTCTCTGA 314
DB 186 ATGTCGTGAAGACTACGAAGATGTATGGCGTGAGATTCAGATTCAGATCATCTCTCTGA 245
QY 315 GCATCCAAATGTTGTTAGGATCAAGGGACTTATGAAGATTCGCTGTTGTTTCATATTGT 374
DB 246 GCATCCTAAATGTTGTTAGATCAAGGGTACTTATGAAGACTCTGTTTTTGTTCACATTGT 305
QY 375 TATGAGGTTTGTGAAGTGGTGAGCTTTTGTGATCGGATGTTTCTTAAAGGTCATTATAG 434
DB 306 TATGGAAGTTTGTGAAGTGGTGAGCTTTTGTGATCGGATGTTTCTTAAAGGTCATTATAG 365
QY 435 TGAGCGTGAAGCTGTCACGCTTATTAAGACGATTCCTTGGTGTGTTGTTGAGGCTTGCTTC 494
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Db 366 TGAACGTGAAGCTGCTAAAGTGAATTAAGACTATTCCTGGTGTGTTGAGGCTTGTCTATC 425
QY 495 TCTTGTGTTATGATAGAGATCTAAACCTGAGAAATTTCTTGTGATAGTCTCTAAAGA 554
Db 426 TCTTGTGTTATGATAGAGATCTTAAGCTGAGAAATTTCTTGTGATAGTCCAGTGA 485
QY 555 TGATGCTAAGCTTAAGGCTACCGATTTTGGTTTGTCTGTCTCTATAAGCCAGGACAATA 614
Db 486 TGATGCTAAGCTTAAGGCTACAGACTTTGGTTTGTCTGTCTCTATAAGCCAGGCGAGTA 545
QY 615 TTTATATGAGTGTAGTGGAGTCCGTACATATCTTGACACAGAGAGTCTAAGAAATGTTA 674
Db 546 TCTGTATGATGTAGTGGAGTCCGTATATGTTGACCTGAGGTTCTGAAGAAATGTTA 605
QY 675 TGGACCTGAATATAGATGTGGGAGTGTGCTGTATCTCTACATTTTACTCAGCGGTGT 734
Db 606 TGAACACAGATAGAGCTGTGGAGCCGCTGTATCTGTATCATCTTACTAAGTGGGGT 665
QY 735 TCTTCCCTTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATGCAAGGGAAGTT 794
Db 666 TCTCTCTTTTGGGCAGAAACCGAGTCAGGAATCTTTAGGCAGATATGCAAGGGAAGAT 725
QY 795 AGATTTCAAAATCTGACCCGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCTATAA 854
Db 726 AGATTTTAAATCTGATCCGTGGCTACTATCTCAGAGGTCGTAAGATTTGATTTACAA 785
QY 855 AATGCTGAAAGGAGCCGCCAAGAACCATTTCTGCTCATGAAGCCTTGTGTCAACCATG 914
Db 786 AATGCTGATAGAGCCGCCAAGAACCTATTTCTGCACATGAAGCATGTGTCAACCTTG 845
QY 915 GATTTCCGATGACACAGCAGACAGCAAGCCTTTCATCCAGCAGTCTTATCTCTCT 974
Db 846 GATTTGTATGAACATCTGACACAGCAAGCCTTCTGACCCAGCAGTCTTGTGCGGACT 905
QY 975 AAGACGTTTCTCAAAATGAATTAAGATTAAGAAATGSGCATTTAGCGGTAAATGCTGAG 1034
Db 906 TAAGCAGTCTCGCAATGAATTAATTAAGAAATGSGCATTTAGCGGTAAATGCTGAG 965
QY 1035 ACTTTCAGAGGAATTAAGTGTCTGAGGCTGTAAGGAAATTTCAAGATGATAGACAGACAA 1094
Db 966 ACTTTCAGAGGAATTAAGTGTCTGAGGAAATTTCAAGATGATAGACAGACAA 1025
QY 1095 CAGGGAACCATTTCTTGAAGAGCTCAAGCGGTTTGAAGAGATCGGATCTGAAT 1154
Db 1026 CAGTGGAAACATCACCTTTGAAGAGCTTAAAGCAGGCTTAAAGAGAGTTGGATCTGAAT 1085
QY 1155 GATGGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGAACACAGTGTGTAAT 1214
Db 1086 GATGGAATCAGAAATCAAGTCTCTTAAGGATGCGGCTGATATCGAACACAGTGTGTAAT 1145
QY 1215 AGACTACGAGAAATCTCAGCAGCAACCTTACACATGAACAGATGAGAGAGAGAGAT 1274
Db 1146 AGACTACGAGTGAATCTCAGCAGCAACCTTACATATAAAGATGAGAGAGAGAGAGAA 1205
QY 1275 TCTGTTGGCTGCAATTTCTGGACTTTGACAAGAGCGGAGCGGTTATATCAACATCGATGA 1334
Db 1206 CTGTTGGTGTGCGTTTCTATCTTTGATAAGATGGTAGCGGTTATATCAACATGACGA 1265
QY 1335 GCTTACGCTGTCAGAGAGTTGGTCTATGTATACACCTCTGACACATGATGATCAA 1394
Db 1266 GCTTCAACAAGCCCTGCACAGATTTGCTCTGTGACACTCTCTTGTATGACATGATCAA 1325
QY 1395 GGATTTGATCTTGACAAATCAGCGGAAGATCGATTTCTCGAGTTTACACATGATGAG 1454
Db 1326 AGATTTGATCTTGATTAATCAGCGGAAGATTTGATTTCTCAGAGTTTACTGCTGATGAA 1385
QY 1455 GAAAGGAGTGGAGTTGGGAGAGCAGACCAATGATGAAGAACTTGAACATTCACATTCG 1514
Db 1386 GAAAGGAGTGGTGTGGGAGGAGCAGAACTATGAGGAACAACTTGAATTCATATAGC 1445
QY 1515 TGATGCTTTTGGAGTTGATG 1534
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Db 1446 TGAAGCTTTTGGAGTTGAGG 1465

RESULT 4

AAF74274

ID AAF74274 standard; DNA; 1768 BP.

XX AAF74274;

AC AC

XX DT

XX 04-MAY-2001 (first entry)

XX

DE Soybean calcium dependent protein kinase clone #2.

XX

KW Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat; diquat; crop production; ds.

XX

OS Glycine max.

XX

PN WO200107592-A2.

XX

XX 01-FEB-2001.

XX

XX 26-JUL-2000; 2000WO-GB02876.

XX

PR 27-JUL-1999; 99GB-0017642.

XX

PA (ZENE) ZENECA LTD.

XX

PI Holt CD, White AJ, Michael AJ, Osborn RW;

XX

DR WPI; 2001-168549/17.

XX

Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole

XX Claim 18; Page 37; 50pp; English.

XX

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

XX Sequence 1768 BP; 511 A; 325 C; 464 G; 468 T; 0 other;

SQ

Query Match 43.3%; Score 756.4; DB 22; Length 1768;
Best Local Similarity 70.6%; Pred. No. 1.6e-161;
Matches 1009; Conservative 0; Mismatches 421; Indels 0; Gaps 0;

QY 106 GTTCTACCATATCAACACACCGATTAAAGATCATTTACCTTCTGGGAAAAAGCTAGGC 165

Db 195 GTTCTCCCGCAGCGCAGCAACATCCGTGAGGTGTACGAGGTGGCGGAAAGCTCGGG 254

QY 166 CAAGGCAATTTGGAACAACCTATCTGACACAGAGAAATCAACCTCCGCTAATTACGCC 225

Db 255 CAGGCGCAATTCGGACCACTTCGAGTGACCGCGCTCGAGTGGTGGGAAGTTCGCG 314

QY 226 TGAATTCGATCCGAGGAAAGCTGTTGTGCGGAGGATTACGAAGATGATGCGGT 285

Db 315 TGAAGTCGATTCGGAAGCGGAAGCTGCTGTGCAAGGAGGACTACGAGGACGTGTGCGG 374

QY 286 GAGATTCAGATCATCATCTCTGACATCCAAATGTTGTTAGGATCAAGGACT 345

Db 375 GAGATTCAGATCAATGACCACTTGTGGAACACGCCAACGTTTCCGCAATCGAAGGAGC 434

QY 346 TATGAGATTCGGTGTGTTGTTTCATATTGTTATGGAGTTTGTCAAGTGTGAGCTTTT 405

Db 435 TAGAGGATTCACGCCGCTGACCTGGTCATGAGTTGTGCGAGGTGGAGATGTTT 494

QY 406 GATCGGATTTCTTAAAGTCAATTTTGTAGCGGTGAAGCTGTCAAGCTTATTAAGACG 465

Db 495 GACAGGATCGTGAAGAGGAGGACACTACAGCGAGAGACAGCGCGAGGTGTGATAAGACG 554

QY 466 ATTCTTGCTGTTGTTAGGCTTGTCATCTCTTGTTGTTGTTATGATAGATCTCAAACTT 525
Db 555 ATTTGTTGAGTGTGTTAGGCTGTCACCTGCTAGGCTGTCATAGGCTTAAAGCTT 614
QY 526 GAGAAATTCCTGTTGTTAGTTCCTTAAGATATGCTAGCTTAAGCTTACGATTTGGT 585
Db 615 GAGAAATTCCTGTTGTTAGTTCCTTAAGATATGCTAGCTTAAGCTTACGATTTGGT 674
QY 586 TTGCTGCTCTTCTTAAGCCAGGCAATATTATATGATGCTAGTGTGGAAGTCCGTAAT 645
Db 675 TTGCTGCTCTTCTTAAGCCAGGCAATATTATATGATGCTAGTGTGGAAGTCCGTAAT 734
QY 646 GTTCAGCAGAGGCTGCTAAAGAAATGTTATGACCTGAAATAGATGTGGAAGTCTGGT 705
Db 735 GTTCAGCAGAGGCTGCTAAAGAAATGTTATGACCTGAAATAGATGTGGAAGTCTGGT 794
QY 706 GTTATCTCTCTACATTTTACTCAGGGTGTCTCTCTCTCTGCGCAGACAGCTGCTGGA 765
Db 795 GTTATCTCTCTACATTTTACTCAGGGTGTCTCTCTCTCTGCGCAGACAGCTGCTGGA 854
QY 766 ATCTTTAGCAGATATTGCAAGGAAGTTAGATTTCAATCTGACCCGTGGCTACTATC 825
Db 855 ATCTTTAGCAGATATTGCAAGGAAGTTAGATTTCAATCTGACCCGTGGCTACTATC 914
QY 826 TCAGAAGCTGCTAAAGATTTGATCTATATAAATGCTGGAAGGAGCCCAAGAAAGCAAT 885
Db 915 TCAGAAGCTGCTAAAGATTTGATCTATATAAATGCTGGAAGGAGCCCAAGAAAGCAAT 974
QY 886 TCTGCTCAATGAGGCTTGTGTCACCCATGCTGTCGATGAACAGCAGCAGCAGCAAG 945
Db 975 ACAGCAGATGAGTACTCGGCCACCCATGCTGTCGATGAACAGCAGCAGCAGCAAG 1034
QY 946 CTTCTGATCAGCAGCTTCTATCTGCTGCTAAAGCAAGTTTCTCAATGAATTAAGTAA 1005
Db 1035 CTTCTGATCAGCAGCTTCTATCTGCTGCTAAAGCAAGTTTCTCAATGAATTAAGTAA 1094
QY 1006 AAAATGGCATTACGGTAAATGCTGAGAGCTTTCAGAGGAGAAATGGAGGCTGGA 1065
Db 1095 AAGATGGCATTACGGTAAATGCTGAGAGCTTTCAGAGGAGAAATGGAGGCTGGA 1154
QY 1066 GAATGTTCAAGATGATAGACACAGACAAACGAGCAAGTACTTTTGAAGAGCTCAA 1125
Db 1155 GAGTATTCAAGATGATAGACACAGACAAACGAGCAAGTACTTTTGAAGAGCTCAA 1214
QY 1126 GCGGTTTGAAGAGCTGAGTCTCACTGATGATGAATCAGAAATCAAGTCTCTATGAT 1185
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QY 1186 GCGGCTGATATCGACACAGTGTGTACATAGACTACGAGAAATCTAGCAGCAACCTTA 1245
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QY 1246 CACATGACAGATGGAGAGAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1305
Db 1335 CATTAAATAAGCTGGAGAGAGAGAGAACTAGTGTGGCTTCTCTCTATTTTGAACAA 1394
QY 1306 GACGAGAGGCTTATATCACCATGATGATGATGATGATGATGATGATGATGATGAT 1365
Db 1395 GATGAGAGTGTGATATACCTTGTATGATGATGATGATGATGATGATGATGATGAT 1454
QY 1366 TGTATACACCTCTGAGGAGATGATCAAGGAGATGATGATGATGATGATGATGATGAT 1425
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QY 1426 GATTTCTGGAGTTTACAGCAATGATGAGAAAGAGATGAGTGGGAGAGCAGAAC 1485
Db 1515 GATTTCTGGAGTTTACAGCAATGATGAGAAAGAGATGAGTGGGAGAGCAGAAC 1574
QY 1486 ATGATGAGAGCTTCACTTCAACATGCTGATGCTTTTGGAGTTGATGG 1535
Db 1575 ATGAGAAACACATAATTAAGAGATGCTCTTGGATGATGATGATGATGATGATGATGAT

RESULT 5

AA42924
ID AAC42924 standard; DNA; 1671 BP.
XX
AC AAC42924;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37370.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
25-FEB-2000; 2000EP-0301439.
XX
25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
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PR 22-OCT-1999; 99US-0160981.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 39.4%; Score 688.4; DB 21; Length 1671;
 Best Local Similarity 67.2%; Pred. No. 3.8e-146;
 Matches 974; Conservative 0; Mismatches 476; Indels 0; Gaps 0;

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QY 73 ACGAAGCCAAACCCCTAGACGCTCTTCAACACACAGTTCTACCATATCAACACACGATTA 132
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Db 220 ATGAGCGGTAAACCCACACATCAAGCTTACTATGTTCTTGGTCATTAAGACACCAACATT 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 133 AGAGATCATTCCTTCTGGGAAAAAAGAGTAGGCCAAGGCCAATTTGGAACAACTATCTC 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 280 CGTGATATCTATACCTCTAGCCCAAGCTAGGTCACAGGTCATTTGGAACGACTTATCTA 339
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QY 193 TGCACAGAGAAATCAACCTCCCGCTTAATTCAGGCTGAAATCGATCCGAGGAAAGCTC 252
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Db 340 TGTACAGAGATTGCCTCAGGCGTTGACTAGGCTTGTGAAGTCAATATCCAGAGAGAGTTG 399
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Qy 253 GTGTCGCGAGGATTCAGAAAGATGTATGGGTGAGATTTCAGATCATCATCTCTCT 312
 Db 400 ATCTCTAAGAAAGATGTTGAGGATGTTAGAAAGGAGATTCAGATAATCATCATTTAGCT 459
 Qy 313 GAGCATCAAAATGTTTGTAGGATCAAGGACTTATGAGGATTCGGTGTGTTTCATATT 372
 Db 460 GGTACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519
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 Qy 433 ATGAGCGTGAAGCTGTCAAGCTTATTAAGAGATTCCTGTTGTTGTTGTTGTTGTTGTT 492
 Db 580 AGTGAGAGAAAGCTGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 639
 Qy 493 TCCTTGTGTTATCATAGAGATCTCAAGCTGAGATTTCTTCTTCTTCTTCTTCTTCTTCT 552
 Db 640 TCGCTGTGTTATCATAGAGATCTCAAGCTGAGATTTCTTCTTCTTCTTCTTCTTCTTCT 699
 Qy 553 GATGATGCTTAAGCTTAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 612
 Db 700 GATGATGCTTCTCAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 759
 Qy 613 TATTTATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
 Db 760 ATATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
 Qy 673 TATGAGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
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 Qy 793 TTGATTTCAAAATCTGACCGTGTCTATCTCTCAAGAGCTGCTCAAGATTTGATCTAT 852
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 Qy 853 AAAATGCTGAAAGAGCCCAAGAAACGATTTCTGCTCATGAGCCCTGTGTCACCA 912
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 Qy 913 TGGATTTGATGAAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 972
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 Qy 973 CTAAAGAGTTTCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1032
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 Qy 1033 AGACTTTCAGAGAAATGAGCTGCTCAAGGATTTCTCAAGATGATGATGATGATGATGATGAT 1092
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 Qy 1093 AACAGCGGAAACGATTTACTTTTGAAGAGCTCAAAAGCGGTTTGAAGAGAGCTGATCTGAA 1152
 Db 1240 AACAGCGGAAACGATTTACTTTTGAAGAGCTCAAAAGCGGTTTGAAGAGAGCTGATCTGAA 1299
 Qy 1153 CTGATGGAATCAGAAATCAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1212
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 Qy 1273 ATCTGTGTGCTGATTTTCTGAGTCTTTCAGAAAGAGCGGTTTATATCACCATCGAT 1332
 Db 1420 CATCTTGTGAGGTTTCTCAATATTTTGAACAAGATGGAAGCGGTTTCTATCAACAAATGAT 1479

Qy 1333 GAGCTTCAGTTCAGCTTCACAGAGTTTGGTCTATGTATGATACACCTCTCGACGACATGATC 1392
 Db 1480 GAGCTTACAAAGCGTGTGTTGAACATGCGATGCGTGTGTTTCTTGAAGACATCATC 1539
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 Db 1540 AAGGAGATTGATTCGACAATGACGGGAAGATCGATTTCCTCGAGTTTACAGCAATGATG 1599
 Qy 1453 AGGAAAGAGATGAGTTGGGGAAGAGCAACCATGATGAGAACTTGAACCTCAACATTT 1512
 Db 1600 CAAGAAGGAAATGCTGTTGGTGAAGAGGACGATGAGAAATAGTCTAAACATTTAGCATG 1659
 Qy 1513 GCTGATGCTT 1522
 Db 1660 AGAGACGCGT 1669

RESULT 6
 AAF74283
 ID AAF74283 standard; DNA; 2550 BP.
 XX AAF74283;
 AC AAF74283;
 DT 04-MAY-2001 (first entry)
 XX Cucurbita pepo calcium dependent protein kinase clone.
 DE Cucurbita pepo calcium dependent protein kinase clone.
 XX Calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; ds.
 XX Cucurbita pepo.
 XX WO200107592-A2.
 PN 01-FEB-2001.
 PD 26-JUL-2000; 2000WO-GB02876.
 PF 27-JUL-1999; 99GB-0017642.
 PR (ZENE) ZENECA LTD.
 XX Holt CD, White AJ, Michael AJ, Osborn RW;
 PI WPI; 2001-168549/17.
 DR Producing herbicide resistance plants by inhibiting calcium dependent
 PT protein kinase in plants or by providing an intracellular vacuolar
 PT transporter capable of transporting agrochemical into plant vacuole
 XX Claim 18; Page 43; 50pp; English.
 XX The present invention describes a method of producing plants which are
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those
 CC plants which are resistant to the agrochemical of interest. This is
 CC useful in the production of crops with herbicide resistance.
 XX Sequence 2550 BP; 710 A; 467 C; 627 G; 746 T; 0 other;
 SQ

Query Match 37.4%; Score 652.6; DB 22; Length 2550;
 Best Local Similarity 66.6%; Pred. No. 5.5e-138;
 Matches 934; Conservative 0; Mismatches 469; Indels 0; Gaps 0;

Qy 67 ATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126
 Db 843 ATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 902
 Qy 127 CGATTAGAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 186
 Db 903 AACTTTAAGGAGGATTTATGAGCTTGGGTAAATAAATAGGCCAAGGACAAATTTGGGACACA 962
 Qy 187 TATCTCTGCACAGAGAAATCAACCTCGCTTAATTTACGCTGCAATGATGCCGAGGAGCA 246

Db 963 TATATGTGTGGAGAAAGCAACTGGAAAGAGTATGCTGTGAAGTCTATTGCAAAAGAG 1022
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Db 1023 AAGTGGTTAATGAGATGATGTTGAAGATGTGAGAAGGAATTCAGATAATGCACCAT 1082
QY 307 CTCCTGAGCATCCAAATGTTGTAGATCAAAAGGAGCATATGAGATTCGGGTGTTGTT 366
Db 1083 TTGCTGTGGACACCGGAATGTTATATCATCAAGGGGGCGGTACGAGGATCCGTTGCAGTT 1142
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Db 1143 CAGGTAGTCAAGAGTGTGTGTCGAGGTGAGCTATTGATAGGATCAATCAACGTGGA 1202
QY 427 CATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAAGCAGATTCCTGGTGTGTTGAGGCT 486
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Db 1323 AAGGAGAGCAATCACTTCTCAAGACAATGATTGAGACTATCAATGTTCTTCAACCA 1382
QY 607 GGCACATATTATGACGTAGTGTGAAGTCCGTACTATGTTGCACGAGGTCGTAAG 666
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QY 667 AATGTTATGGACCTGAATAGATGTGTGAGTGTCTGCTTATCTCTTACTATTTACT 726
Db 1443 AAGCATATGTCAGAAAGCAGATGTTGGAGTGTGCTGGAGTAATGTATACATCTCTTA 1502
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QY 1087 ACAGACACAGCGGACGATTTCTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCCGA 1146
Db 1863 ACTGACACAGCGGCCAAATCACATTTTGAAGAACTCAAGCTGGAATTTGAAGTTTGA 1922
QY 1147 TCTGAACCTGATGGAATCAGAATCAAGTCTCTCATGATGCGGTGATATCGACAACAGT 1206
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QY 1207 GGTACAATAGACTACGGAGAATTTCTTAGCAGCAACCTTTACACATGAACAAGATGAGAGA 1266
Db 1983 GGAACCATCGACTAGCGGGAGTTCGTAGCTGCCATTTGCATCTAAACAAAATCGAAG 2042
QY 1267 GAGGAGATCTTGGTGGCTGCAATTTTCGACCTTTGACAAGACGGAACGGGTTTATATCAC 1326

Db 2043 GAAGATCATCTTCTAGCAGCGTTTTCATATTTTCGACAAAGATGGAGCGGTTTCATTACC 2102
QY 1327 ATCGATGAGCTTCAGTCACTTGCACAGAGTTTGGTCTATGATACACCTCTGGAGCAGC 1386
Db 2103 CACGACGAGCTTCAACAAGCATCTAAAGAGTTTGGGATAGAGGATCTTCAATGGAAGAA 2162
QY 1387 ATGATCAAGGAGATTCATCTTGACATGACGGGAAGATCGNTTCTCGGAGTTTACAGCA 1446
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QY 1447 ATGATGAGGAAGAGAGATGGAGT 1469
Db 2223 ATGATCAAAAGGAATGTAGT 2245
RESULT 7
ID AAF74285
XX AAF74285 standard; DNA; 2022 BP.
AC AAF74285;
XX AC
XX DT
XX 04-MAY-2001 (first entry)
XX Vigna radiata calcium dependent protein kinase clone.
XX DE
XX Vigna radiata calcium dependent protein kinase; CDPK; herbicide resistance;
XX KW
XX paraquat; diquat; crop production; ds.
XX OS
XX Vigna radiata.
XX PN
XX WO200107592-A2.
XX PD
XX 01-FEB-2001.
XX PF
XX 26-JUL-2000; 2000WO-GB02876.
XX PR
XX 27-JUL-1999; 99GB-0017642.
XX PA
XX (ZENE) ZENECA LTD.
XX PI
XX Holt CD, White AJ, Michael AJ, Osborn RW;
XX DR
XX WPI; 2001-168549/17.
XX PS
XX Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole -
XX CC
XX Claim 18; Page 44-45; 50pp; English.
XX CC
XX The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

XX SQ
XX Sequence 2022 BP; 587 A; 374 C; 466 G; 595 T; 0 other;

Query Match 36.1%; Score 629.8; DB 22; Length 2022;
Best Local Similarity 65.3%; Pred. No. 7.5e-133;
Matches 925; Conservative 0; Mismatches 492; Indels 0; Gaps 0;

QY 116 ATCAACACACCGATTAAGAGATCATTCACCTCTGCGAAGAAAGCTAGGCGCAAGCCAAAT 175
Db 140 ATAAGACTCCCAACATTCGTGATCTATACACTCTTGGCGCAAAATGGGACAGGGAAT 199
QY 176 TTGGAACAACCTATCTCTGACAGAGAAATCAACTCGCTAATACGCTGCAAAATCGA 235
Db 200 TTGCAACCACTTATTTATGCAACCGAGAAATCTACTTCAATGAATATGCTGCAAAATCTA 259
QY 236 TCCGAGAGCGAAGCTCGTGTGTCGAGGATTAAGAGATGATGCGTGTGAGATTCAGA 295
Db 260 TCTCCAAAGAAAGTGTGATTTCCCAAGGAGGATGTTGAGATGTCCAGAGGGAATTCAGA 319

Qy	296	TCATGCATCATCTCTCTGAGCATCCAAATGTTTGTAGGATCAAAGGGACTTTATGAAGATT	355
Db	320	TAAAGCAATATTTAGCTGGTCAAGAACAATTTGTCACCAATTAAGGTCGCTTACGAGATC	379
Qy	356	CGGTGTTTGTTCATATTTGTTATGGAGGTTTGTGAAGGTGGTGAGCTTTTGTATCGGATTG	415
Db	380	CTCTCTATGTGCATATAGTCATGGAGCTTTGTTCTGGGGTGAGTGTGTTGATCGCATCA	439
Qy	416	TTTCTAAAGTGCATTTTAGTGACCGTGAAGCTGTCAAGCTTATTAAGACGATTCCTGGTG	475
Db	440	TCAGAGGGGCCACTATACGAGAGGAAGCGCTGCAGAGTTGACCAAAATTTATTTGGGG	499
Qy	476	TTGTTGAGGCTTGTCATTCTCTTGTGTTTATGCATAGAGATCTCAAAGCTCAGAAATTCCT	535
Db	500	TTGTTGAGGCTTGTCATTCCCTTGGGTCATGCCACAGAGATCTCAAGCCAGAAAACITTC	559
Qy	536	TGTTTGATGTCCTAAAGATGATGCTTAAGCTTAAAGGCTACCGATTTTGGTTTGTCTGCT	595
Db	560	TTTGTGTCATAAAGATGATGATTTCTCTCTTAAAGCAATTGACTTTGGCCTCTCCGTTT	619
Qy	596	TCATTAAGCCAGACAAATATTTATATGACGTAGTTGGAGTCCGTFACCTATGTTCCACAG	655
Db	620	TCCTCAACCCGTCAAATTTTCACTGATGTAGTCGGCAGGCCATACCTATGTTGCTCCTG	679
Qy	656	AGGTGCTAAAGAAATGTTATGGACCTGAAATAGATGTGTGGAGTCTGGTGTATTCCTCT	715
Db	680	AGGTTCTCCTCAAGCACTATGGCCCTGAAGCAGACGTGTGGACAGCCGCTGTCATACGT	739
Qy	716	ACATTTTACTCAGCGTGTTCTCCCTTCTGGGCAGACACTGAGTCTGGAACTTTTAGAC	775
Db	740	ACATATTTGCTTATGTGTACCAACATTTTGGCAGACACCCACAAGGTATATTTGATG	799
Qy	776	AGATATTGAAGGGAAGTTAGATTTCAAATCTGACCCGTGGCTACTATCTCAGAAAGCTG	835
Db	800	CAGTATTGAAGGCACATATAGATTTTGACTCAGATCCCTTGGCCTCTAATATCTGACAGTG	859
Qy	836	CTAAAGATTGATCTATAAATGTCTCGAAGGAGCCCAAGAACGCAATTTCTGCTCATG	895
Db	860	GAAAAGATCTGATCAGAAAGATGCTGTGTTCTCAGCCCTTCAGAGCGTTGACTGCTCATC	919
Qy	896	AAGCCTTGCTCACCATGGATTGTCGATGAACAGCAGCACCAGACAGCCTCTTGATC	955
Db	920	AAGTGTTATGTCATCTTGGATGTGAATTTGGAGTTTGCACCTTGACAGGCAATAGACC	979
Qy	956	CAGAGCTTTATCTCTCTFAAGCAGTTTCTCAAAATGAATTAAGATTAAGAAAAATGGCAT	1015
Db	980	CTGCTGTCTTCTCTCTCTTAAACAGTTTCTTGCATCAATGAATGAAGAAGATGGCAT	1039
Qy	1016	TACGGGTAAATGCTGAGACACTTCAGAGGAAGAATTTGGAGTCTGAAGAATTTGTCA	1075
Db	1040	TGCGGGTGATGCTGAAGCTCTATCUGAAGAGGAGATTCTGGATTGAGAGAAATGTTTC	1099
Qy	1076	AGATGATAGACAGACAAACAGCGGAACGATTACTTTTGAAGGCTCAAAGCGGTTTGA	1135
Db	1100	AGGCTATGGATACCGATAACAGTGGTGAATCACATTTTGTATGAATCAAAGCTGCTTAA	1159
Qy	1136	AGAGGTTCGATCTGAACCTGATGGAATCAGAATCAAGTCTCTCATGTATCGGCTGATA	1195
Db	1160	GAGATATGTTCTTACCCCTTAAAGATGTAGAATACGTTGATCTGATGAAGCGGCTCATG	1219
Qy	1196	TCGACACAGTGGTACAAATAGACTACGGAGAATTCCTAGCAGCAACCTTACACATGAACA	1255
Db	1220	TCGACAAAAGTGCACCAATAGATTATGGGAGCTTTATTTGCTGTACAGTCTCATCAACA	1279
Qy	1256	AGATGGAGAGAGAGATATCTGGTGGCTGCAATTTTCGGACTTTGACAAAGACGGAAGC	1315
Db	1280	AAGTCAAGCTGAAGAACATCTTATTTGACGCAATTCCAATATTTTGAACAGGATGGCAGT	1339
Qy	1316	GTTATATCACCATCTGATGAGTTCAGTCAAGCTGACAGAGTTTGGTCTATGTGATACAC	1375
Db	1340	GTTATATACGGTTGATGACTTTCACAAGCTTTGTGCAGAACATTAACATGACTGATGCTT	1399

[illegible]

RESULT 8	
AAC45753	
ID	AAC45753 standard; DNA; 3054 BP.
XX	
AC	AAC45753;
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 47639.
XX	
KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EPI033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	23-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	23-APR-1999; 99US-0130891.
PR	28-APR-1999; 99US-0131449.
PR	30-APR-1999; 99US-0132048.
PR	30-APR-1999; 99US-0132407.
PR	04-MAY-1999; 99US-0132484.
PR	05-MAY-1999; 99US-0132485.
PR	06-MAY-1999; 99US-0132486.
PR	06-MAY-1999; 99US-0132487.
PR	07-MAY-1999; 99US-0132863.
PR	11-MAY-1999; 99US-0134256.
PR	14-MAY-1999; 99US-0134258.
PR	14-MAY-1999; 99US-0134219.
PR	14-MAY-1999; 99US-0134221.
PR	14-MAY-1999; 99US-0134370.
PR	18-MAY-1999; 99US-0134768.
PR	19-MAY-1999; 99US-0134941.
PR	20-MAY-1999; 99US-0135134.
PR	21-MAY-1999; 99US-0135353.
PR	24-MAY-1999; 99US-0135629.
PR	25-MAY-1999; 99US-0136021.
PR	27-MAY-1999; 99US-0136392.
PR	28-MAY-1999; 99US-0136782.
PR	01-JUN-1999; 99US-0137222.
PR	03-JUN-1999; 99US-0137528.
PR	04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143342.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 18-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149802.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 34.2%; Score 597.4; DB 21; Length 3054;
Best Local Similarity 63.6%;
Matches 947; Conservative 0; Mismatches 506; Indels 36; Gaps 1;

QY	63	AAAAATGGAGACGAAGCCAAAACCCCTAGACGTCCTCTCAAACACACAGTTTCCACATATCAAAAC	122
Db	1554	ACATATGAGGAGAGTGTCCAGTGCAGGGCTTAGAACTCAGTCAGTGTTCGAGAGGAAAC	1613
QY	123	ACCACAGTTTAAGAGATCATACCTTCTGGGAAAAGCTAGGCCAAGGCCAAATTTGGAAC	182
Db	1614	TGAAAACCTTTAAGGAGTCTATTTCATTAGGGAGGAACTTGGACAAGGCAATTTGGGAC	1673
QY	183	AACTATCTCTGCACAGAGAAATCAACCTCCGCTAAATACGCCCTGCAAAATCGATCCCGAA	242
Db	1674	GACGTTTTATGCCTTGCAAAAGGTACTGGGAACGAATATGCGTGCAAGTCGATTTCCAA	1733
QY	243	GCAAAAGCTCGTGTGTGTCGGCAGGATACGAAGATGTATGGCGTGAGATTCAGATCATGCA	302
Db	1734	GAGGAAGCTTTTGACCTGATGAGGATGTTGAAGATGTGAAGAGAGAGATTCAGATAATGCA	1793
QY	303	TCATCTCTGAGCATCCAAAATGTTGTAGGATCAAAAGGACTTATGAAGATTCGGTGTT	362
Db	1794	TCACTTGGCTGGTCATCCGAATGTTATATCTATTAAGAGTGCTTATGAGGATGTTGTGC	1853
QY	363	TGTTTCATATTGTTATGGAGGTTTGTGAAGGTGGTGAGCTTTTGTATCGGATTTGTTCTAA	422
Db	1854	GGTACATCTTGTGATGGAGTTGTGTTCGGGTGGCGAGCTTTTGTATAGAAATTTTCAACG	1913
QY	423	AGTCAATTTTAGTGACGCTGAAGCTGTCAAGCTTATTAAGACGATCTTGGTGTTGTGA	482
Db	1914	TGGACATTAACCTGAGAGAAAAGCTGCTGAGCTTCGGAGAACCATTGTGGGGTTTTAGA	1973
QY	483	GGCTTGTCACTCTCTTGGTTGTTATGCATAGACATCTCAAACTCAGAAATTTCTTGTTTGA	542
Db	1974	GGCTTGTCACTCTCTTGGTTGTTATGCATCGGAACCTCAAGCCAGAAATTTCTATTTGT	2033
QY	543	TAGTCTTAAGAPGATGCTAAAGCTTAAGCTTACCAGTTTGGTTGCTGCTCTCTATAA	602
Db	2034	TAGTAGAGGAAGATTCCTGTGTAAAAACGATGACATTTGGACTCTCAATGTTCTTTAA	2093
QY	603	GCAGGACAAATATTTATATGAGCTAGTTGGAGTCCGTACTATGTTGCACCAGAGGTCT	662
Db	2094	GCAGATGAGGTTTTTACAGATGTTGTGGTAGTCGCTATTATGTAGTCCAGAAAGTTCT	2153
QY	663	AAAGAAATGTTATGGACCTGAAATAGATGTGPGAGTGTGGTGTTATCCCTCTACATTTT	722
Db	2154	TAGAAAGCGTTAIGGTCCTGAATCAGATGTGGAGTGTGGTGATGTTTACATATTT	2213
QY	723	ACTCAGGGTGTTCTCCCTCTCGGG-----	748
Db	2214	GTTAAGCGGAGTTTCCCTCTTTTTCGGCGCGCTCTGAACTAAATTTGTTTCCATGAATA	2273
QY	749	--CAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAATC	806
Db	2274	TACAGAACGGAACAGGATATTTTCGAGCAGTCTCTCATGAGATCTGTGATTTTCATC	2333
QY	807	TGACCCGTGGCCTACTATCTCAGAGCTGCTTAAGATTTGATCTATAAATGCTCGAAAG	866
Db	2334	TGATCCATGGCCCAAGCACTCTCAAAAGCCGAAAGACTTGGTAAGGAAAATGCTTTGTTCG	2393
QY	867	GAGCCCCAAGAACCGATTTCTGCTCATGAAAGCTTGTGTCACCCATGGATGTGCAATGA	926
Db	2394	AGACCCCAAGCGAAGACTAACCGACATCAAGATATATGTCTATCCATGGGTACAGATTGA	2453
QY	927	ACRAGACGACACAGAACGCTCTTGATCCAGCAGTCTTATCTCGTCTCTAAAGCAGTTTTC	986
Db	2454	CGGTGTGGCTCCAGATAAACCTCTGCACTCTGCTGTCTGAGCCGTATGAGCAATTTTC	2513
QY	987	TCAATGAATTAAGATTAAAGAAATGGCATTTACGGGTAAATTGCTGAGAGACTTTCAGAGGA	1046
Db	2514	TGCAATGAACAAGTTCAAGAAAATGSCCTCTTAGAGTCTATGCTGAGAGCTTATCTGAAGA	2573
QY	1047	AGAAATTTGAGGTTCTGAAGGAATTTGTTCAAGATGTAGACACAGACACACACGGGAACAT	1106
Db	2574	AGAAATAGCCGGTTTTAAACAAATGTTCAAGATGATAGACGACAGACAATAGTGGTTCAGAT	2633

Qy	1107	TAC	TTTTGAAGAGCTCA	AAGCGGGTTTGAAGAGAGATCGGATCTGAAC	TGATGGAATCAGA	1166
Db	2634	CAC	TTTTGAAGAAGTGA	AGACGAGACTAAACGAGTGTGTC	CAATCTCAAGAGATCAGA	2693
Qy	1167	AAT	CAAGTCTCATGAT	CGCGCTCATATCGACAAACAGTGGTACAATAGACTAC	GAGAGA	1226
Db	2694	GAT	CTTTGATCTAATG	CAAGCTCTGATGTGGACAAATACCGGAACGATAGACTAC	ACAAGA	2753
Qy	1227	ATT	CTAGCAGCAACCTT	ACACATGAAACAAAGATGGAGAGAGAGAGATCTTGGTGGCTGC	1286	
Db	2754	GTT	CATAGCCGCCACAT	TTCATCTAAACAAAATAGAGAGAGAGAGACCAATTTGTTGGCGCG	2813	
Qy	1287	ATT	TTTCGGACTTTCACA	AAAGACGGAAGCGGTTATATACCACTCGATGAGCTTCAGTCAGC	1346	
Db	2814	CTT	CTCTACTTTGACA	AGGACGAGAGTGGCTTTATCACCCGGACGAGCTTCAAC	ANC	2873
Qy	1347	TTG	CACAGAGTTTGGTCT	ATGTGATACACCTCTGGACGACATGATCAAGAGAGATTGATCT	1406	
Db	2874	TTG	CGGAAGAGTTTGGTGT	TGAAGATGCCCGCATAGAAGAAATGATGCGCGATGTTGATCA	2933	
Qy	1407	TGACA	ANTGACGGGAAGATCG	ATTCTCGAGATTTACAGCAATGATGAGAGAAAGAGATGG	1466	
Db	2934	AGACA	AGGATGGAGAAATAG	ACATACACAGATTTGTGGCAATGATGCAAGAAAGGAGCAT	2993	
Qy	1467	AGT	TGGGAGAGCAGAAC	CAATGATGAAGAACTTGAACCTTCAACATTTGCT	1515	
Db	2994	ANT	GGGAGGACCTGTG	AGATGGGTTTAGACAGACCATAGCANTTTCT	3042	
RESULT	9					
AAF74277						
ID	AAF74277	standard; DNA; 2334 BP.				
XX	AC	AAF74277;				
XX	DT	04-MAY-2001 (first entry)				
XX	DE	Rice calcium dependent protein kinase clone #1.				
XX	KW	Calcium dependent protein kinase; CDPK; herbicide resistance;				
XX	OS	paraquat; diquat; crop production; ds.				
XX	PN	Oryza sativa.				
XX	PD	WO200107592-A2.				
XX	PF	01-FEB-2001.				
XX	PR	26-JUL-2000; 2000WO-GH02876.				
XX	PA	27-JUL-1999; 99GB-0017642.				
XX	PI	(ZENE) ZENECA LTD.				
XX	DR	Holt CD, White AJ, Michael AJ, Osborn RW;				
XX	PT	WPI; 2001-168549/17.				
XX	PS	Producing herbicide resistance plants by inhibiting calcium dependent				
XX	CC	protein kinase in plants or by providing an intracellular vacuolar				
XX	CC	transporter capable of transporting agrochemical into plant vacuole				
XX	CC	Claim 18; Page 39; 50pp; English.				
XX	CC	The present invention describes a method of producing plants which are				
XX	CC	resistant to the herbicides paraquat and diquat, involving inhibiting				
XX	CC	the plants a calcium dependent protein kinase (CDPK) and selecting the				
XX	CC	plants which are resistant to the agrochemical of interest. This is				
XX	CC	useful in the production of crops with herbicide resistance.				
XX	SQ	Sequence 2334 BP; 659 A; 430 C; 625 G; 620 T; 0 other;				

Query Match

32.78; Score 571.4; DB 22; Length 2334;

Query Match 32.7% Score 571.4; DB 22; Length 2334;

Best Local Similarity 62.2%; Pred. No. 1.3e-119;
Matches 899; Conservative 0; Mismatches 546; Indels 0; Gaps 0;

Qy 91 COTCCTTCAACACAGTCTTACCATATCAAAACACACAGCATTAAGAGATCAATACCTTCTG 150
Db 531 CTTACATCTATCAATGCTTGGGGGAGACACGGGACCTTAAGGAGCATATATCATNT 590
Qy 151 GGAAGAAAGCTAGGCGCAAGGCAATTTGGACACAGCTATCTCTGACAGAGAAATCAACC 210
Db 591 GGTGGAAGCTTGGTCAGGCCAGTTTGGCACAACTTACCTCTGTACCGAGATCAATACA 650
Qy 211 TCCGCTAATAGCCCTGCAATCGATCCGAGCGAAGAGCTCGTGTGCGGAGGATTAAC 270
Db 651 GGGTGTAGTATGCTTGAAGACCATCCAAAGCGAGCTCATCCCAAGGAGATGTA 710
Qy 271 GAAGATGTATGCGGAGATTCAGATCATGTCATCTCTCTGAGCATCCCAATTTGTT 330
Db 711 GAAGATGTGCGGCTGAGATTCAGATCATGTCATCTCTCTGAGCATCCCAATTTGTT 770
Qy 331 AGGATCAAGGAGCTTATGAAGATTCGGTGTGTTTTCATATTTATGAGAGTTTGTGAA 390
Db 771 GCAATCAAGGATGTCTATGAGATGGCAAGCGGTGCACATTTGTATGAGCTCTCGCT 830
Qy 391 GGTGAGCTTTTGTATCGGATTTCTTAAAGGTCTATTTAGTGAAGCTGAAGCTGTC 450
Db 831 GGTGAGCTTTTGTATCGGATTTCTTAAAGGTCTATTTAGTGAAGCTGAAGCTGTC 890
Qy 451 AAGCTTATTAAGACGATTTCTGCTGTGTTGAGGCTTGTCTATCTCTGCTGTTATGCAAT 510
Db 891 GAGCTTAAAGAAATATTTCTCTCTATTAAGCCAGGACATATTTATATGAGCTAGTT 570
Qy 511 AGAGATCTCAACCTGAGATTTCTTGTGTTGATGCTTAAAGATGATGCTAGCTTAAAG 570
Db 951 CGTGATCTTAAAGCAAGAAATTTCTCTCTATTAAGCCAGGACATATTTATATGAGCTAGTT 1010
Qy 571 GTCACGATTTGCTGTCTCTCTATTAAGCCAGGACATATTTATATGAGCTAGTT 630
Db 1011 GCAATAGATTTGCTGTCTCTCTATTAAGCCAGGACATATTTATATGAGCTAGTT 1070
Qy 631 GGAAGTCCGCTATGTTGACACAGAGTGCTTAAAGAAATGTTATGAGCTCAAAATAGAT 690
Db 1071 GGGAGTCCATATATCTCTCTGAGTATTGACAAACGTTATGAGCAGAAATCTGAT 1130
Qy 691 GTGTGAGTCTGCTTATCTCTACATTTTACACAGGCTTCTCTCTCTCTCTCTCTCTCT 750
Db 1131 GTGTGAGTCTGCTTATCTCTACATTTTACACAGGCTTCTCTCTCTCTCTCTCTCTCT 1190
Qy 751 GAGACTGAGTCTGGAATCTTACAGATATTTGCAAGGAAATGATTTTCAATCTGAC 810
Db 1191 GAGACACACAGGATATTTGATGAGTCTTGAAGGTCACATTTTCAATCTGAT 1250
Qy 811 CCGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCTAATAATGCTGCAAGAGGC 870
Db 1251 CCATGGCAAGATATCTGACAGTGAAGGATCTTATAGAAATGCTCTCTCTCTCTCT 1310
Qy 871 CCCAAGAGGCTTCTGCTCATGAGCTTGTGTCACCCATGAGTGTGCGATGAACAA 930
Db 1311 CTTTGGAGGCTTGAAGGCCCATGAGTGTGTCAGGATCTTGGATCTGTGAATGGA 1370
Qy 931 GCAGCACACAGAGCTCTTGTATCCAGCATCTTATCTCTCTTAAAGCAGTTTCTCAA 990
Db 1371 GTTGCCACTGATCAAGCTCTGGATCCAGGTTATCTCTCTCTCAAAATCTCTGCA 1430
Qy 991 ATGATTAAGATTAAGAAATGCTTACGAGTAAATGCTGAGAGCTTTTCAAGGAGAA 1050
Db 1431 ATGAAAGATTAAGAAATGCTTACGAGTAAATGCTGAGAGCTTTTCAAGGAGAG 1490
Qy 1051 ATTGGAGCTGAGGAAATGTTCAAGATGATGACACAGACACAGGCAAGATTAAT 1110
Db 1491 ATTGCTGGTTAAGAGAAATGTTCAAGGAGTGGACACAAATATAGGTTGATCACT 1550
Qy 1111 TTTGAGAGCTCAAGCGGTTTGAAGAGAGTGGATCTGAATGATGGAATCAGAAATC 1170

Db 1551 TTCGCTGAGCTTACAGAGGTTTAAAGAGATTTGGCGCTGAATTTAAGGATACAGAGATT 1610
Qy 1171 AAGTCTCTATGATGGGCTGATATCGACAAACAGTGGTACAAATAGACTACGGAGATTC 1230
Db 1611 GGTGATATATGGAAGCGGCACACAGCAATAATTAACAATCCATTAAGAAGAAATT 1670
Qy 1231 CTACAGCAACCTTACACATGAACAAGATGGAGAGAGAGATTCGTTGGCTGCAATT 1290
Db 1671 AATGCTGCAATCTACCTCTTAAACAAGATGAAGCTGAGGAGCAGCTCTGCGAGCTTTT 1730
Qy 1291 TCGGACTTTGACAAAGACGAGGCTTATATCACCATCGATGAGCTTCACTAGCTTGC 1350
Db 1731 ACATATTTGACAAAGATGGGAGTGGTATATCAGAGTTGACAAGCTTCAACGAGCTTGT 1790
Qy 1351 ACAGAGTTTGGCTATGATACACCTCTGACGACATGATCAAGAGATTTGACTTGAC 1410
Db 1791 GGAGAACATACATGAGGATTCACCTCTGAGAGATTTTTCAGAGGTTGATCAAAAC 1850
Qy 1411 AATGACGGAAGATCGATTTCTCGAGTTTACAGCAATGATGAGGAAAGGAGATGGAGTT 1470
Db 1851 AATGACGCGCAATTTGATGACTACCGCAATTTGAGCCATGATGCAAGGAGCAAGCTTGA 1910
Qy 1471 GGGAGACGACAAACCATGATGAGAACTTGAACCTTCAACATTTGATGCTTTTGGAGTT 1530
Db 1911 CTAGGTTGGCAACAATGGAAGCAGTTTGAATGTAGCATTAAGAGAGCGCACCTCAAGTA 1970
Qy 1531 GATGG 1535
Db 1971 CATTTG 1975

RESULT 10
AAF74275
ID AAF74275 standard; DNA; 1910 BP.
XX
AC AAF74275;
XX
DT 04-MAY-2001 (first entry)
XX
DE Sweet potato calcium dependent protein kinase clone.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX
OS Ipomoea batatas.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
PR 27-JUL-1999; 99GB-0017642.
XX
PA (ZENE) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
DR WPI; 2001-168549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX
PS Claim 18; Page 38; 50pp; English.
XX
CC The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX
SQ Sequence 1910 BP; 560 A; 348 C; 481 G; 521 T; 0 other;

Query Match 30.7%; Score 537.2; DB 22; Length 1910;
Best local similarity 63.2%; Pred. No. 6.8e-112;
Matches 843; Conservative 0; Mismatches 488; Indels 3; Gaps 1;

QY 131 TAAGAGATCATTTACCTTCCTGGGAAAGAAAGTAGGCCAAGCCAAATTTGGAACAACTATC 190
DB 308 TTAGGGCACTTACACTCTGGGAAAGAAAGTAGGGTAGGGTCAATTTGGGGTTTACCTATT 367
QY 191 TCTGCACAGAAATCAACTCGCTCAATTTACGCCCTGCAAAATCGATCCGGAAGCGAAGC 250
DB 368 TGTCTACTGAGATTGAACTGGAAGCAGTATGCCCTGCAAGTCAATTTCCAGAAAGAGC 427
QY 251 TCGTGTCTCCGAGGATTACGAAGATGTATGGCGTGAGATTTTCATGATCATCATCTCT 310
DB 428 TTGTGCTAAGGGGATAGAGATGATATGAGGAGGAGGTTTCAGATTTATGCAACCTTGA 487
QY 311 CTGAGCATCCAAATGTTGTAGGATCAAGGGGACTTTATGAAGATTCGGTCTTTGTTCAVA 370
DB 488 GTGGCAGCCTATATTTGTAGTTCAAGGGGCTTTATGAGGATGCTAATCTCTGTATC 547
QY 371 TTTTATGAGGTTTCTGAAGGTGGTGGCTTTTTCATGCGATTGTTTCTAAAGGTCAIT 430
DB 548 TTCTGATGAGTTGTGTGCTGGTGGAGAGCTTTTCGATCGGATTTATGCTAAGGGCACT 607
QY 431 TTAGTCAGCGTGAAGCTGTCAAGCTTAATTAAGACGATTTCTGTGTTTGTGAGCGTTGTC 490
DB 608 ATAGCGAAAGGGCTGTGCTCTCTTTGTCAGGTCTTATAGTGAATGTTGTTTCACTATGCC 667
QY 491 ATTCTCTGTGTGTTATGCTAGAGATCTCAAACTCAGAAATTTCTGTTTGTATAGTCCCTA 550
DB 668 ATTTTATGGCGTATGACCCGCGATTTGAGCCCGAGAAATTTCTGTTGCTGTGATAAAA 727
QY 551 AAGATGATGCTAAGCTTAAGGCTACCGATTTTGGTTTGTCTGCTTCTTAATTAAGCCAGGAC 610
DB 728 CTGAAATGCTGCTTGAAGGCTACTGATTTTGGCTTATCAGTGTTCATTGAAGAGGAA 787
QY 611 AATATTATATGACGTAGTGTGAAGTCCGCTACTATGTTGCACAGAGGCTTAAGAAAT 670
DB 788 GGGTGTATAAGGATTTAGTGGGAGGCTTACTATGTTGCTCCGAGCTTTGGGGAGAA 847
QY 671 GTTATGACCTGAAATAGATGCTGGAGTCTGCTGTTTATCTCTACATTTTACTCAGCG 730
DB 848 AGTATGGGAGGAGCGGATTTTGGAGTCCAGTCTTAATGTTCTATATTTTACTCAGTG 907
QY 731 GTGTTCTCCCTCTGGGAGAGACGTGAGTCTGGAATCTTTAGACAGATTTGCAAGGGA 790
DB 908 GTGTGCTCCCTCTCTGGGCTGAAACTGAGCGGGGATCTTTAATGCTATATACTTTAAAGGAG 967
QY 791 AGTTAGATTTCAATCTGACCCGTGGCTACTATCTCAGAGCTGCTTAAGATTTGATCT 850
DB 968 AACTCGACTTCCAAACGAAACCTTGGCCCTCTATATCGAGCATTTGCCAAGGACCTAGTAC 1027
QY 851 ATAAATGCTCGAAAGSAGGCCCAAGAACGCAATTTCTGCTCATGAGCCCTTGTGTCAAC 910
DB 1028 GAGGGATGCTAGCCCAAGACCCGAGAGAGCGCTTACTGCTGCCAGGTTCTTGAGCATC 1087
QY 911 CATGGATTGCTGATGAACAGACGACCCAGAACGCTCTGTATCCAGAGCTTTATCTC 970
DB 1088 CATGGATGCGAGAAGATGGAGAAGCATCTGCACAGACCCTAGATAGCGCTGTTCTCTCAA 1147
QY 971 GTCTTAAGCAGTTTCTCTCAATCAATGAATTAAGAAATGGCATTTACGGTAAATGCTG 1030
DB 1148 GAATGAAGCAATTCAGAGCAATGAACAACTCAAGAACTTGGCCCTGAAGTTTATTCAG 1207
QY 1031 AGAGCTTTTCAGAGAAAGAAATTTGGAGCTCTGAAGGAATTTGTTCAAGATGATACACAG 1090
DB 1208 AAATCTCTCAGAGASAAATTCATGGACTGAAGCAATGTTCCAGAAATTCGACACTG 1267
QY 1091 ACAACAGGCAAGATTTACTTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTGGATCTG 1150
DB 1268 ACAACAGTGGTACAATTACATACGAAGCACTGAAGAGAGGATTTGGCCCACTCGGGGCAA 1327

QY 1151 AACTGTGAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGACAAACAGTGGTA 1210
DB 1328 ATCTCACAGAGGCTGAAGTTAAGCAGTTGATGAAGCTGCTGATGTAGATGGAATGGCT 1387
QY 1211 CANTAGACTACGAGAAATTCCTAGCAGCACTTACACATGAACAAGATGGAGAGAGG 1270
DB 1388 CGATAGACTACATCGGAATTCATCACTGCTACAATGCACAGCACAGGCTAGAAGAGAAG 1447
QY 1271 AGATTCTGCTGGCTGCAATTTTCGAGCTTTGACAAAGCAAGGAGCGTTATATCACCATCG 1330
DB 1448 AATATCTATACAAGCATTTTCAGTATTTTCATAAAGATAGCAGTGGATTTATCAGAGAG 1507
QY 1331 ATGAGCTTCAGTCAGCTTGCACAGAGTTTGGTCTATGTGTAT---ACACCTCTCGAGACA 1387
DB 1508 ATGAACCTAGAGAGTCTGATGAAGGAACACAGGAATAGCTGATGCAAGCACTATATAAGGAAA 1567
QY 1388 TGATCAAGGAGATGATCTTGACAATGACGGGAAGATTCGATTTCTCGGATTTTACAGCAA 1447
DB 1568 TATATCTGAGTCGATGCAGATCATGAGGAAGATCACTATGAGAGATTTTGCACAA 1627
QY 1448 TGATGAGGAAGGA 1461
DB 1628 TGATGAGATCAGGA 1641

RESULT 11
ABA91081
ID ABA91081 standard; cdNA; 2230 BP.
XX
AC ABA91081;
XX
DT 22-FEB-2002 (first entry)
XX
DE Physcomitrella patens CPK-2 full-length cdNA, SEQ ID NO:26.
XX
KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
KW PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
KW PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
KW casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
KW MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
KW MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
KW calcium-dependent protein kinase-2; CPK-2; overexpression;
KW environmental stress; salinity; drought; temperature; tolerance;
KW transgenic plant; EST; expressed sequence tag; ss.
XX
OS Physcomitrella patens.
XX
PN WO200177356-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US11435.
XX
PR 07-APR-2000; 2000US-196001P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Da Costa Silva EO, Bohnert HJ, Van Thielens N, Chen R;
PI Sarria-Millan R;
XX
DR WPI: 2002-049153/06.
DR P-PSDB; AAM52842.
XX
PT New protein, useful for increasing tolerance to environmental stress,
PT comprises a Protein Kinase Stress-Related Protein selected from
PT Protein kinases, Casein Kinase homologs, MAP kinases or Calcium
PT dependent protein kinases
PS Claim 14; Fig 2M; 154pp; English.
XX
XX Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA

sequences were obtained from expressed sequence tags (ESTs: AB91056-AB91068) derived from *Physcomitrella patens* cDNA libraries. The PKSRPs of the invention comprise protein kinase-6 (PK-6), protein kinase-7 (PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2), MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5), calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer tolerance to environmental stresses such as salinity, drought, temperature, metal, chemical, pathogenic and oxidative stress. *Physcomitrella patens* PKSRP nucleic acids may be used to generate transgenic plants and seeds with increased tolerance to salinity, drought and temperature. The transgenic plants generated can be monocots or dicots and are especially maize, wheat, rice, oat, triticale, rice, barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants (e.g., soybean, peanut, *Vicia* species, alfalfa), solanaceous plants (e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grasses and forage crops. The PKSRP nucleotide and proteins may also be used in evolutionary and protein structural studies and as markers for specific regions of the genome.

Sequence 2230 BP; 572 A; 477 C; 661 G; 520 T; 0 other;

Query Match 30.4%; Score 531.8; DB 24; Length 2230;
Best Local Similarity 62.5%; Pred. No. 1.2e-110;
Matches 849; Conservative 0; Mismatches 507; Indels 3; Gaps 1;

141 TTACCTCTGGGAAAAAGCTAGCCCAAGCCCAATTTGGACACACCTATCTTCGCACAGA 200
142 TTTACCTCTGGGAAAAAGCTAGCCCAAGCCCAATTTGGACACACCTATCTTCGCACAGA 200
602 TTTACCTCTGGGAAAAAGCTAGCCCAAGCCCAATTTGGACACACCTATCTTCGCACAGA 661
201 GAAATCAACCTCCGCTAATTAACGCTGCAATCGATCCGCAAGCGAAGCTCGTGTGCG 260
662 CAGATGACGAATGAGCGCTACGCTGCAAGACATCGCCCAACGGAACCTGACCAGTAA 721
261 CGAGGATGACGAATGAGCGCTACGCTGCAAGACATCGCCCAACGGAACCTGACCAGTAA 721
722 GGAGGATGACGAATGAGCGCTACGCTGCAAGACATCGCCCAACGGAACCTGACCAGTAA 781
321 AAATGTTGTTAGGATCAAGGAGCTTAAGAGATCGGCTGTTGTTCAATATCTTATGGA 380
782 CAAATGCTGGTGTAAAGGATGTTGTCAGGACAGCATTCGTCGATCTTGTGATGGA 841
381 GGTGTTGAGAGTGGTGGAGCTTTTGAATCGGATGTTTCAAGGTCATTTTATGAGAGC 440
842 GCTCTGTGAGTGGGAGCTCTTCGATCGATCATCATTCGCAAGGGGCAATACAGTGAAG 901
441 TGAAGCTGTCAAGCTTATTAAGAGATCTTGGTGTGTTGAGCTTGTCTCTCTTGG 500
902 CGCCGCTGCGGATGTCAGAGTCTATGTCGTCATGTCGTCGTCGTCGTCGTCGTCGTC 961
501 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 560
962 GATCTTCCATCGGATCTCAAGCCAGAGATTTTCTGTCGTCGTCGTCGTCGTCGTCGTC 1021
561 TAGCTTAAAGCTACCGATTTTGGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 620
1022 GCCTCTGAAGGCCACAGACTTCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1081
621 TGAGGATGTTGGAAGTCCGCTACTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 680
1082 GGATGTTGTTGGAAGTCCGCTACTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1141
681 TGAATATGATGTTGGAAGTCCGCTACTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 740
1142 TGAAGCTGATGTTGGAAGTCCGCTACTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1201
741 CTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 800
1202 CTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1261

801 CAAATCTGACCGTGGCTACTATCTCAGAGCTGCTAAAGATTTTGTATCTATATAAATGCT 860
1262 CGAAGACGATCCATGCGCGGAAATCTCCACGCGGCTTAGAATTTGGTGGGAAATGCT 1321
861 CGAAGAGGCCCCAAGAAAGCGATTTTGTCTCATGAAGCTTGTGTACCCATGATGATG 920
1322 AAACCCCTAAGCTGAAGATAGTCTGACGGCAGCAGAGGTTTGAACCATCCATGGATGAA 1381
921 CGATGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 980
1382 GGAAGATGTTGATGCTCCAGAGCTGCCACTCGACATGCGGTTTGAACCATGATGAA 1441
981 GTTTCTCAATCAATTAAGATTAAGAAATGCGCATTAACGGTAAATGCTGAGAGATTTT 1040
1442 TTTCTAGCGCCCAACAAGATGAAGAGTGGCGCTCAAGTCAAGTCAAGTCAAGTCAAG 1501
1041 AGAGAGAAATTTGAGGCTTCAAGAAATTTTCAAGATGATAGACACAGCAGCAGCAG 1100
1502 GGAGGAGAGATGCTGGGTTGAGGAGATTTTCAATCCATAGATACAGACAGCAGCAG 1561
1101 AACGATTAATTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCCGATCTGAATGATGGA 1160
1562 CACGGTACGCTTCGAGAGCTTAAGAAAGGTTGCTGAAGCAGGGCTCAAAATCTTAATGA 1521
1161 ATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGACACAGCTGGTCAATAGACTA 1220
1622 ATCGGACATCAGGAAACTAATGAAGCTGAGATGCTGATGGAACGCGCAAGATCGACT 1681
1221 CGGAGATCTTAGCAGCAGCTTACACATGAACAGATGAGAGAGAGAGATCTCTGGT 1280
1682 CAACGAGTTCATATCGGCAACATGACATGAACAGAGCGGAGAGAGATCACCTTTG 1741
1281 GGTGATCTTTGAGCTTTGACAAAGCGGAGCTTATATCACCATGATGAGCTTCA 1340
1742 GGAGCATTCATCAATTCGACAGCAGCATACGCGGTATATCACCATGACAGCTTCA 1801
1341 GTCAGCTGACAGAGTTGGTCTATGTATAC---ACCTCTGAGCAGCATGATCAAGGA 1397
1802 GGAAGCAATGGAGAAATGGAATGGAGATCTGAGACCATCCAGAGATCATCAGCGA 1861
1398 GATTGATCTTGAATGACGCGGAGATCGATTTCTCGAGTTTACAGCAATGATGAGGA 1457
1862 GTTGGACACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1921
1458 AGGAGATGAGTTGGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1496
1922 GGGCAATCTGCGCTGAAACGAGGAGCGGTGAACAA 1960

RESULT 12

AAF74281
ID AAF74281 standard; DNA; 1647 BP.

XX AAF74281;

XX AAF74281;

DT 04-MAY-2001 (first entry)

XX

DE Liverwort calcium dependent protein kinase clone #1.

XX Calcium dependent protein kinase; CDPK; herbicide resistance;

KW paraquat; diquat; crop production; ds.

XX Marchantia polymorpha.

OS

XX

PN WO200107592-A2.

XX 01-FEB-2001.

XX 26-JUL-2000; 2000WO-GB02876.

XX 27-JUL-1999; 99GB-0017642.

XX (ZENE) ZENPCA LTD.

XX PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX DR WPI; 2001-168549/17.
XX PT Producing herbicide resistance plants by inhibiting calcium dependent
XX PT protein kinase in plants or by providing an intracellular vacuolar
XX PT transporter capable of transporting agrochemical into plant vacuole
XX PS Claim 18; Page 42; 50pp; English.
XX CC The present invention describes a method of producing plants which are
XX CC resistant to the herbicides paraquat and diquat, involving inhibiting in
XX CC the plants a calcium dependent protein kinase (CDPK) and selecting those
XX CC plants which are resistant to the agrochemical of interest. This is
XX CC useful in the production of crops with herbicide resistance.
XX SQ Sequence 1647 BP; 447 A; 349 C; 465 G; 386 T; 0 other;
Query Match 29.9%; Score 523; DB 22; Length 1647;
Best Local Similarity 62.7%; Pred. No. 1.1e-108;
Matches 830; Conservative 0; Mismatches 490; Indels 3; Gaps 1;
QY 141 TTACTTCTGGAAAAAGCTAGGCCAAGCCCAATTTGGAAACACCTATCTCTGCACAGA 200
DB 240 TTACACCTCGGCGGGAACCTGGTCTGGTCTGATGCTGACGCAATTTGTGTACGCA 299
QY 201 GAAATCAACCTCCGCTAATTAGCCCTGCAATTCGATCCGGAAGCGAAAGCTCGTGTGCG 260
DB 300 CAAGGTTACAGTGAGCTTTAGCCCTGCAAGTCAATTCGGAAGAGAGTTGACCAATAA 359
QY 261 CGAGGATTACGAAGATGATGGCGTGAGATTGAGATCATCATCTCTCTGAGCATCC 320
DB 360 GGATCAAGCTAGAGGATGTTGGAGGGAAGTGCAGATCATGCCACCTTAGAGGGGCGAA 419
QY 321 AAATGTTTGGATCAAGGACCTATCAAGATTCGGTGTGTTGTTATGTTATGGA 380
DB 420 GAACATTTGCGAATTTGAAGGGGCGCTATGAGGATTAACACAACTGCTCTGTCATGGA 479
QY 381 GGTGTTGTAAGGTGATGAGCTTTTGTGATCGGATTTCTTAAAGGTCAATTTTGTAGTGGG 440
DB 480 GCTTTGTGCTGCGGAGACCTTCGACCGCATTTATCAGCGGGCCCATCAGTGTAGAG 539
QY 441 TGAAGCTGTCAAGCTTATTAGACGATTTGTTGGTGTGTTGAGGCTGTGTCATCTCTGG 500
DB 540 GSGTGTGCTGAGCTCTATGTAGAACTATAGTCAAGTGTGTCAGAGTGTGCAATCTCTGG 599
QY 501 TGTATGATAGATCTCAACCTGAGAAATTTCTGTTGATAGTCTCTAAAGATGATGC 560
DB 600 AGTTATGACCGGGATCTGAGCCGGAATTTCTGTTGATAGTCTCTAAAGATGATGC 659
QY 561 TAAGCTTAAGGCTACCGATTTTGGTGTGCTCTCTTCTATAAGCCAGGACAATATTATA 620
DB 660 ACCCTGAGGCGAGGATTTTGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 719
QY 621 TGAGTGTGGAAGTCCGCTACTATGTTCCACGAGGCTGCTAAAGAAATGTTATGGACC 680
DB 720 AGATATCGTTGGAAGTCTGCTACTAGTGGCCAGGAGTTTTCGCTGCTGCTGCTGCTGCT 779
QY 681 TGAATAGATGTTGGAGTGGTGTGTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 740
DB 780 AGAGGCTGATGTTGGAGTGGGAGTCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 839
QY 741 CTCTGGGAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATT 800
DB 840 TTCTGGGAGAACCGACACAGGATTTTGTATGCCGTAATGCAGGTCATATTGATT 899
QY 801 CAAATCTGACCGTGGCTTACTATCTCAGAGCTGCTAAAGATTTGATCTATAAATGCT 860
DB 900 CACTAGTGTCTTGGCTTCAATTTCTCAAAGGCGAAAGATCTGCTAAAGAGGATGCT 959
QY 861 CGAAGGAGCCCAAGAACGCAATTTCTGCTCATGAGCCCTTGTCTCACCCTGATGCT 920

DB 960 CAAACAGAACCCAAAGGAGGAGATTGACGGCCCATGAAGTTTAAAGTCAACCATGATTAG 1019
QY 921 CGATGAACAAGCAGCAGCAGCAAGCCTCTGTGATCCAGCAGCTWTATCTCTCTAAAGCA 980
DB 1020 TGTTCGGAGAGCAGCAGCAGCAAAACCATCTGACAAACCGCTGTGCTAGATTGAAGCA 1079
QY 981 GTTTTCTCAAAATGAATTAAGATAAGAAATGCGATTAAGGGTAATTTGCTGAGACACTTTC 1040
DB 1080 ATTCACCGCTATGAACAGCTCAAGAACTTGTCTCTGAAGGTTATCGCAGAGACTCTTC 1139
QY 1041 AGAGGAAGAAATTCAGTCTGAAGGAATTTCTCAAGATGATGACACACACACAGCGG 1100
DB 1140 TGAAGAGAGATCATGGGATTGAAGGAGATGTTTGAAGATGAGCAGACACACAGTGG 1199
QY 1101 AACGATTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCCGATCTGAACTGATGGA 1160
DB 1200 TACAATCACGTTTCGAGGAGTTGAAGGATGCTCTTCAAAAGCAGGATCAAAACCTGGCAGA 1259
QY 1161 ATCAGAAATCAAGTCTCTCATGATGGGCTGATATCCACACAGTGGTACAAATAGACTA 1220
DB 1260 GTCAGAAATGCGGAGCTTAATGGCAGCTGTGATGTGATGGAATGGCATTATTGACTA 1319
QY 1221 CGGAAATTCCTAGCAGCAACCTTACATGAAACAGATGGAGAGAGAGATTTCTGGT 1280
DB 1320 CTGGAGTTTATACCGCAACCATCCACTTGAATGAATAGAGAGGAGATCATCTTTA 1379
QY 1281 GGTGCTATTTTGGGACTTTGACAAAGCGAAGCGGTTATATFACCATCTGATGACCTTCA 1340
DB 1380 CGCTCCCTTTCAGCATTTTGTATGAGCAGCAGCTGGTTCATCACCATGGAGAGCTTGA 1439
QY 1341 GTCAGCTTGCACAGAGTTTGGTCTATGTGATAC---ACTCTGGACGACATGATCAAGGA 1397
DB 1440 ACAGGCTTTAATTAAGCAGCGGATGGGATCCCTGATCTCTGAAAGAAATTTATTAGGA 1499
QY 1398 GATTCATCTTGACAATGACGGAAGATCGATTCTCGGAGTTTACAGCAATGATGAGGA 1457
DB 1500 GGTTCACACTGATCATGATGGACGATCACTACACGAGTTCGTTGCCATGATCGTAA 1559
QY 1458 AGG 1460
DB 1560 AGG 1562

RESULT 13

AAAF74270

ID AAF74270 standard; DNA; 1791 BP.

XX AAF74270;

XX 04-MAY-2001 (first entry)

DE Carrot calcium dependent protein kinase clone.

KW Calcium dependent protein kinase; CDPK; herbicide resistance;

KW paraquat; diquat; crop production; ds.

OS Daucus carota.

PN WO200107592-A2.

XX 01-FEB-2001.

PF 26-JUL-2000; 2000WO-GB02876.

XX 27-JUL-1999; 99GB-0017642.

XX (ZENE) ZENECA LTD.

XX Holt CD, White AJ, Michael AJ, Osborn RW;

XX WPI; 2001-168549/17.

XX Producing herbicide resistance plants by inhibiting calcium dependent

Db 1031 GACCTTGTTAGAAAGATGCTGCACACAGGATCCAGGAGAGGATTACTTCTGCACAAGTT 1090

PT transporter capable of transporting agrochemical into plant vacuole

AA Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
AA

Claim 18; Page 43-44; 50pp; English.

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

Sequence 2363 BP; 718 A; 435 C; 542 G; 568 T; 0 other;

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Query Match      29.9%; Score 521.6; DB 22; Length 2363;
Best Local Similarity 60.3%; Pred. No. 2.5e-108;
Matches 898; Conservative 0; Mismatches 584; Indels 6; Gaps 2.
```

QY	74	CGAAGCCAAACCCCTAGACGCTCTTCACACACACAGCTTCTACCATATATCAAAACACCACGATTA	133
Db	523	CAAAACAGCCCCAAAAGTTGAGCCAAATACAATTTTGGGTAAACCCTTTGAGGATGCA	582
QY	134	GAGATCAATTACCTTCTGGGAAAAGAGCTAGGCCAAGCCAAATTTGGAACAACCTATCTCT	193
Db	583	AGGTGTACTACATTTGGGAGAGAACTGGGTAGGGGTCAATTTGGGGTTTACCTATCTCT	642
QY	194	GCACAGAGAAATCAACCTCCGCTTAATTAGCCCTGCAAATCGATCCCGAAGGAAAGCTCG	253
Db	643	GCACGACAAAAGAGCTGGGCCAACAAATATGCTTGCAAGTCAATCTCTAAGAAGAAGCTTG	702
QY	254	TGTGTGCGAGAGATTACGAGATGTTATGGCGTGAGATTCAGATCATGCAATCATCTCTGT	313
Db	703	TGACC AAGGCTGATAAGGATGATACGAGAGAGAGATTCAGATCATGCAAGCATATGAGTG	762
QY	314	AGCATCCAAATGTTTGTAGGATCAAAAGGACATTATCAAGATTCCGGTGTGTTGTTTCATATTG	373
Db	763	GTCAACCTACATTTGTTGGAATTTAAGGGTGCTTATGGAGTAAACATCTGTGAATCTTG	822
QY	374	TTATGAGGTTTGTGAAGGTGGTGAGCTTTTGTATGCGGATTTGTTCTAAAGCTCATTTTA	433
Db	823	TGATGAGGCTTTGTGCTGTGTGGGGATCTTTTGATAGGATTTATGCTAAGGGGCATTATA	882
QY	434	GTCAAGCTGAAGCTGTCAAGCTTATTAAACAGCATTTCTGGTGTGTTGAGGCTTGTCAATT	493
Db	883	GTCAAAAGGCTGCTGCCCATGTGTTGAGGCGAGATTTTAATGTTGTTCACTGTGTCACAT	942
QY	494	CTCTTGGTGTATGCATAGAGATCTCAAAACCTGAGCAATTTCTGTTGATAGTCTCAAG	553
Db	943	TTATGGGTGTGATGCATAGGATCTGAAGCCCTGAGAATCTTCTGCTCTACCAAGGATG	1002
QY	554	ATGATCTTAAGCTTTAGGCTACCGATTTTGGTTTGTCTGCTCTCTATAGCCAGGACAAT	613
Db	1003	AGAAATCTCTTTGAAGGCCATGATTTTGGGTTGTCTGTGTTATGGAAGAAGTAAG	1062
QY	614	ATTATATACATAGTTTGAAGTCCGTAATGTTTGCACGAGGTCGTAAAGAAATGTT	673
Db	1063	TCTACCGGATATAGTAGGACGTCTACTATGTCGCTCGAGTATTCGTCGTAGT	1122
QY	674	ATGGACTCAATAGATGTGTGAGTGCTGGTGTGTTATCCTCFACATTTTACTCAGCGGTG	733
Db	1123	ATGGGAAGGAGATGTGATGTTTGGAGTCTGGAATCATGTTGTACATCTTACTCAGTGGTG	1182
QY	734	TTCTCTCCCTCTGGGCAGAGACTGAGTCFGAATCTTTAGACAGATATTGCAAGGGAATG	793
Db	1183	TGCCCCCTTTTGGGCAGAAACGGAGAAGGATCTTTGATGCTATTTTTCGAAGGCCATA	1242
QY	794	TAGATTTCAAACTGACCCGTGGCTTACTATCTCAGAAGCTGCTAAAGATTTTGATCTATA	853
Db	1243	TTGATTTGAAAGCAAAACCATGGCCATCAATTTCAATGGTGCCAAAGGACCTTAGTGAA	1302
QY	854	AAATGCTGAAAGGAGCCCCAAGAAGCATTTCTGCTCATGAAGCCCTTGTCACCAT	913
Db	1303	AAATGTTGACACAGGATCCCAAGAACGATTACTGCTGCTCAAGTTCTTGAGCACCAT	1362
QY	914	GGATTTGATGAACAAGCAGCACCAAGACCCCTCTTGATCCACGAGTCTTATCTGTGTC	973

Db	1363	GGCTAAGAGATGGTGAAGCAT---CAGACAAGCCAAATAGACACTGCTGCTTCTCTCAGGA	1419
QY	974	TAAAGCAGTTTTCCTCAAATGAATAAGATTAAAGAAATGGCAATTACGGGTAAATTGCTGAGA	1033
Db	1420	TGAAGCAATTCAGAGTCATGAACAACCTCAAGAGCTCGCTCAAAGGTCAATGCTGAA	1479
QY	1034	GACHTTCAGAGGAGAAATTTGGAGGTCTGAAGGAATTTTCAAGATGATAGACAGACA	1093
Db	1480	ATCTTCTCGATGAAGAGATCCAAAGGCTGAAACAATGTTCCGGAATATGCACACTGATG	1539
QY	1094	ACAGCGAAGCAATTTACTTTTGAAGAGCTCAAAGCGGTTTGAAGAGAGCTCGGATCTGAAC	1153
Db	1540	GTAGTGGGTCAATTAACCTATGAAGAAGCTGAGGAGGGATTTGGCTGCACTTGGATCAAGC	1599
QY	1154	TGATGGAATCAGAAATCAAGTCTCTCATGGATCGGGCTGATATCGACAACAGTGGTCAAA	1213
Db	1600	TTACTGAAACTGAAGTGAAGCGCTCATGGAAGCTGCTGATCAAGATGGAATGSGATCAA	1659
QY	1214	TAGACTACGGAGATTCCTTAGCAGCAACCTTACATGAACAGATGGAGAGAGGAGA	1273
Db	1660	TAGACTACTATGATTTCAATTACAGCCACAATGCATAGTACAGGTTACAGAGAGATGAGC	1719
QY	1274	TTCTGTTGCGCTGCATTTTCGGACTTTGACAAAGACGGAGCGGTTATATACCACTCGATG	1333
Db	1720	ATCTTTACAGGCATTCCTAATTTTCGACAAAGACAATAGTGGGTTTATCACACAGATG	1779
QY	1334	AGCTTCAGTCAGCTTGACACAGATTTGGTCTATGTGAT---ACACTCTGGACGACATGA	1390
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QY	1391	TCAAGGAGATTTGATCTTGACATGACGGGAAGATCGATTTCCTCGAGTTTACAGCAATGA	1450
Db	1840	TGTTGGAAGTAGACACTGATATGATGGAAGAATAAATCTATGAGTTTCAGCGCAATGA	1899
QY	1451	TGAGGAAAGAGATGGAGTTGGGAGAAGCAGAACCATGATGAAGAACTTGAACCTTCAACA	1510
Db	1900	TGAGAAGTGGACTCAAAACCCGGTTACAAACTCATTTAGTGCATGTGATTTCTAGCA	1959
QY	1511	TTGCTGATGCTTTTGGAGTTGATGGTGAANAATTCGATGACTGACTCA	1558
Db	1960	CTGTATTAACGTAAACGCTTTTTTAAGTACCAAGGTTATGAACAAGTCA	2007

RESULT 15

RESULT IS
AAF74273
ID AAF74273 standard; DNA; 2436 BP.

AC AAE74273:

DT 04-MAY-2001 (first entry)

DE Soybean calcium dependent protein kinase clone #1.

Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat; diquat; crop production; ds.

OS Glycine max.

XX PN WO200107592-A2.

01-FEB-2001.

26-JUL-2000; 2000WO-GB02876.
AA
PF

PR 27-JUL-1999; 99CB-0017642.

PA (ZENE) ZENeca LTD.

PI Holt CD, White AJ, Michael AJ, Osborn RW;

WPI; 2001-168549/17.

PT Producing herbicide resistance plants by inhibiting calcium dependent

PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX Claim 18; Page 36-37; 50pp; English.

XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.

XX Sequence 2436 BP; 738 A; 435 C; 515 G; 747 T; 1 other;

Query Match 29.8%; Score 520.2; DB 22; Length 2436;
Best Local Similarity 64.5%; Pred. No. 5.2e-108;
Matches 793; Conservative 0; Mismatches 433; Indels 3; Gaps 1;

QY 143 ACCTTCGGGAAAAGCTAGGCCAAGCCAAATTGGAACAACCTATCTCTGCACAGAGA 202
DB 739 ACACACITGGGAAGAGTTGGGTAGAGGGCAATTTGGTGTGACATATCTTTGCACTGAGA 798
QY 203 AATCAACTCCGCTAATTAACCCCTGCAATCGATCCCGAAGCGAAGCTCGTGTGTCGG 262
DB 799 AITCGACCGGATTCAGTATGCCCTGCAAGTCCATTTCCAGAGGAAACTTCCGAGCAAA 858
QY 263 AGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCTCTCTCGAGCATCAA 322
DB 859 CTGATAGGAGGACATGAAGAGGAGATTCAGATATGCGACATTTGAGTGGTCAACCCA 918
QY 323 ATGTTGTTAGGATCAAGAGGACTTATGAGANTCGGTTTGTTCATATGTTATGAGGAG 382
DB 919 ACATTTGTTAGTTCAAAAGGGCTTATGAGGATGAGAGTCAAGTTCATCTTTGATGGAGC 978
QY 383 TTTCTGAGGTGGTGCAGCTTTTCATCGGATGTTTCTAAAGGTCAATTTAGTGCAGCGTG 442
DB 979 TGTGTGAGGTGGGGAATTTTTCATAGGATTTGCAAGGGGCATTCACAGTGAAGG 1038
QY 443 AAGCTGTCAAGCTTATTAAGACGATTTCTTGGTGTGTTGGCTGTGCTATCTCTTGGTG 502
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QY 503 TTATGATAGAGATCTCAAACTCAGAAATTTCTTGTGTGATAGTCCFAAGATGATGCTA 562
DB 1099 TGATGATAGGATCTGAAGACAGAGAAATTTTGTCTATCTAGTAGGGACGAAAAATGCAC 1158
QY 563 AGCTTAAGGTACCGATTTTGGTTGTTGCTCTTCTATAGCCAGACAAATATTTATATG 622
DB 1159 TTCTCAAGGCAACGATTTTGGCTTGTGCTATTTTCATGGAAGGAAAGGTATATCGGG 1218
QY 623 ACGTAGTGAAGTCCGTACTATGTTGCACAGAGGTGCTAAAGAAATGTTATGGAAGCTG 682
DB 1219 ATATAGTGTGATGCTTACTATGTTCTCTGAAGTCTCGCGCGCAGATGTGGGAAGG 1278
QY 683 AAATAGATGTGAGTGTGCTGTTATCTCTACATTTTACTCAGCGGTGTTCCCTCCCT 742
DB 1279 AAATAGATATATGAGTGTGAGGATCATATTTATATCTTACTTATGAGGTCCCTCCAT 1338
QY 743 TCTGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTCGAAGGAAAGTTAGATTCA 802
DB 1339 TTTGGGCTGAGACTGAAGGGAATATTTGATGCCATATTTGGAAGGTCACATTTGATTTG 1398
QY 803 AATCTGACCGGTGCCCTACTATCTCAGAAGCTGCTAAAGATTTGATCTATAAAATGCTCG 862
DB 1399 AAAGTCAACCATGCTTAACATCTCAGACAGTCCAGGATCTTGTTCGTAAGATGCTTA 1458
QY 863 AAAGGAGCCCAAGAACGCAATTTCTGCTATGAAGCCTTGTGTCACCCATGGAATGTCG 922
DB 1459 TACAGGATCCAAAGAAAGCAATTAACCTCTGCTCAAGTCTTGTGAGCACCACATGGAAT 1518
QY 923 ATGAACAGAGCAGCAGACAGAGCTCTTGTATCCAGAGCTTTATCTCGTCTAAAGCAGT 982
DB 1519 ATGGAAA---TGCTTCAGACAAAGCCGATAGACAGTGCAGTCCCTTTCCAGATGAAGCAAT 1575

QY 983 TTTCTCAATGAATTAAGATTAAGAAAATGGCATTTACGGGTAAATTCCTCAGAGACTTTTCAG 1042
DB 1576 TTAGAGCAATGAATTAAGCTAAAGAAACTTGCCTTTGAAGGTCAATTCCTCAGAGAAATGTCG 1635
QY 1043 AGGAAGAAATGGAGGTCTGAAGGAATTTCTCAAGATGATAGACACAGACACAGCGGAA 1102
DB 1636 CAGAGAGATCCCAAGGTTTGAAGCAATGTTACAAATATGGACACTGACAAGAGTGGTA 1695
QY 1103 CGATTACTTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTGGGATCTGAACTGATGAAGAT 1162
DB 1696 CAATCACTATGAAGAACTTAAGTCAGGATTCATAGACTTGGCTCAAGCTTACAGAGG 1755
QY 1163 CAGAAATCAAGTCTCTCATGGATCGGCTGATATCGACACAGTGGTACATAGACTACG 1222
DB 1756 CTGAAGTGAAGCAACTTATGGAAGCTGCTGATGTAGATGGAATGGCTCAATTCAGCTACA 1815
QY 1223 GAGAAATTCCTAGCAGCAACCTTACACATGACACAGATGGAGAGAGAGATTTCTGGTGG 1282
DB 1816 TAGAATTCATCAGTCTACATGATGATGACACACAAATTAAGAAAGAGATGACCAACTTTTCA 1875
QY 1283 CTGCATTTTCGGACTTTTGCACAAAGACGAGCGGTTATATCACCATCGATGAGCTTCAGT 1342
DB 1876 AGGCTTTCCAAATATTTTGAATAAGACACACAGTGGGTTTATACAAAGAGATGAATTTGAAT 1935
QY 1343 CAGCTTGCACAGAGTTTGGTCTATGTGAT 1371
DB 1936 CAGCCATCAAGAAATATGGTATGGTGTAT 1964

Search completed: March 26, 2003, 07:52:20
Job time : 527 secs

GenCore version 5.1.4_p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 23:20:20 : Search time 72 Seconds
(without alignments)
7441.171 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747
Sequence: 1 gatccgggtacattcttc.....tataaaagtgttgaaattcc 1747

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
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- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	429.8	24.6	1349	1	US-07-951-715A-20 Sequence 20, Appl
2	429.8	24.6	1349	2	US-08-459-448A-20 Sequence 20, Appl
3	429.8	24.6	1349	3	US-08-459-595A-20 Sequence 20, Appl
4	429.8	24.6	1349	3	US-08-459-504B-20 Sequence 20, Appl
5	429.8	24.6	1349	3	US-08-459-444-20 Sequence 0, Appl
6	429.8	24.6	1349	4	US-09-547-422-20 Sequence 0, Appl
7	218	12.5	4162	2	US-08-459-448A-26 Sequence 26, Appl
8	218	12.5	4162	3	US-08-459-595A-26 Sequence 26, Appl
9	218	12.5	4162	3	US-08-459-504B-26 Sequence 26, Appl
10	218	12.5	4162	3	US-08-459-444-26 Sequence 26, Appl
11	218	12.5	4162	4	US-09-547-422-26 Sequence 26, Appl
12	218	12.5	4165	1	US-07-951-715A-26 Sequence 3, Appl
13	189.6	10.9	2374	4	US-09-347-801-3 Sequence 1, Appl
14	165	9.4	1400	1	US-08-464-164-1 Sequence 1, Appl
15	165	9.4	1400	1	US-08-338-057-1 Sequence 1, Appl
16	165	9.4	1400	2	US-08-668-416-1 Sequence 10, Appl
17	129.8	7.4	1776	3	US-08-655-352-10 Sequence 10, Appl
18	129.8	7.4	1776	4	US-09-258-016-10 Sequence 10, Appl
19	129.8	7.4	1776	4	US-09-257-825B-10 Sequence 10, Appl
20	117	6.7	2061	4	US-09-800-960-1 Sequence 1, Appl
21	114	6.5	2514	3	US-08-655-352-1 Sequence 1, Appl
22	114	6.5	2514	4	US-09-258-016-1 Sequence 1, Appl
23	114	6.5	2514	4	US-09-257-825B-1 Sequence 1, Appl
24	104.2	6.0	1282	2	US-08-878-989-12 Sequence 12, Appl
25	104.2	6.0	1282	4	US-09-272-796-12 Sequence 12, Appl
26	98.2	5.6	3471	2	US-08-715-568A-2 Sequence 2, Appl
27	92.6	5.3	498	4	US-09-347-801-7 Sequence 7, Appl

Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 9, Appli
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Sequence 36, Appli
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Sequence 3, Appli
Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-07-951-715A-20
; Sequence 20, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlino, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.308
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in Figure 30."
US-07-951-715A-20

Query Match 24.6%; Score 429.8; DB 1; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
QY 290 TTCAGATCATGATCATCTCTCTGAGCATCCAAATGTTGTAGGATCAAAAGGGAGCTTATG 349
Db 1 TGCAGATCATGACCACTCTCCGGCCAGCCACGCTGCTGGGGCTCCGGGGCGCGTACG 60
QY 350 AAGATTCGGTGTGTTTCATATGTTATGAGGTTTGTGAAGGTGTGAGCTTTTGTATC 409
Db 61 AGGACACAGAGAGGGTGTGCTGCTGATGAGCTGTGCGGGGGGGAGCTCTCTCGACC 120
QY 410 GGATGTTTCTAAGGTCATTTAGTACGAGGTGAGCTGTCAAGCTTATTAAGCAGATTC 469
Db 121 GATCATCGCCGGGGCCAGTACACGAGGCGCGCGCGCGGAGCTCTGCGGGCCATCG 180
QY 470 TTGGTGTGTTGAGGCTGTCTCTCTGTTGTTATGATAGAGATCTCAAACTTCGAGA 529
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QY 650 CACGAGGTGCTTAAGAAATGTTATGGACCTGAATATAGTGTGAGTGTGCTGTTA 709
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QY 770 TTAGCAGATATTGCAAGGGAAGTTAGATTTCAAACTGACCGTGGCTTACTATCTCAG 829
Db 481 TCACCGCATCTCTGCGAGGCGACCTTGACCTCTCCAGCGAGCCATGCCACACATCTCGC 540
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QY 1070 TGTTCAGATGATAGACAGACACAGCGGAACGATTTTGTGAGAGCTCAAGCGG 1129

Db 781 TGTTCAAGACATTGCAAGGATAACAGCGGACCATTAACCTCGACGAGCTCAACACG 840
QY 1130 GTTTGAAGAGAGTCGGATCTGAACTGATGAATCAGAAATCAAGTCTCTCATGTATGGG 1189
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QY 1250 TGAACAAGATGGAGAGAGAGAGATTTCTGTGGCTGATTTCCGACTTTGACAAAGACG 1309
Db 961 TGAACAACCTGGATAGAGAGAGAGACCTTTACACAGCAATTCCTGATATTTTCGACAAGACA 1020
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Db 1141 ATTATTCAGATTTTGTGGCATGATGAGGAAAGGAGCGGCTGGTGGCGGACCAATGAACA 1200
QY 1487 TGATGAAGA 1495
Db 1201 TCAAGAAGA 1209

RESULT 2
US-08-459-448A-20
Sequence 20, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merila, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40403
 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8582
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1349 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..1226
 OTHER INFORMATION: /note= "cDNA sequence for maize
 OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
 OTHER INFORMATION: disclosed in Figure 30."
 US-08-459-448A-20

Query Match 24.6%; Score 429.8; DB 2; Length 1349;
 Best Local Similarity 60.3%; Pred. No. 1.4e-99;
 Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
 290 TTCAGATCATCATCTCTCIGAGCATCCAAAGTGTGTAGATCAAGGGACTATG 349
 Db 1 TGCAGATCATCTCCCGGCGAGCCCAACGGTGTGGGCTCCGGCGCGGTACG 60
 350 AAGATTCGGTGTGTTTCATATTTATGAGAGTGTGTGAAGTGTGTGAGCTTTTGTATC 409
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 Db 421 TGCTCTACATCTTCTCGCGCGGTGCTCCCTTCTGGGAGGAGCAAGCAGAGCGCACT 480
 770 TTACAGAGATATTCAGAGGAAGTTAGATTTCAATCTGACCGGTGCCCTACTATCTCAG 829
 Db 481 TCACCGGCATCTCTCGAGGCGAGCTTGACCTCTCCAGCGGACCATGCCACATCTCGC 540
 830 AAGCTGTCTAAGATTTGATCTATAAATGCTCGAAGGAGCCCCCAAGACGATTTCTG 889
 Db 541 CGGAGCCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGG 600

QY 890 CTCATGAAGCCCTTGTCTACCCATGGATTGTCTGAATGAACAAGCAGCAGCAGCAGCCTC 949
 Db 601 COTTCCAGGTCTCTCAATCAACCATGGATCAAGAAGAGCGGAGCGGCTGACACGCCGC 660
 QY 950 TTGATCCAGCAGTCTTATCTGTCTAAGCAGTGTCTTCAATGAATGAATGAATAA 1009
 Db 661 TTGACAACGTTGTCTCGACAGGCTCAAGCAGTTCAGGGCCATGAACGATTCAGAAG 720
 QY 1010 TGGCATTACGGGTAAATGTCTGAGAGACTTTCAGAGGAAGAATTTGAGGCTCTGAAGGAT 1069
 Db 721 CAGCATTGAGGATCAAGCTGGTGCCTATTCGAAGAGGAGATCACAGGCTGAAGGAGA 780
 QY 1070 TGTTCAGATGATGACACAGACACAGCGGAAGGATTTCTTTGAAGAGCTCAAGCGG 1129
 Db 781 TGTTCAGAGCATTTGACAAGGATAACAGCGGAGCCATTACCTCGAGGAGTCAACACG 840
 QY 1130 GTTTCAGAGAGTGGGATCTGAACCTGATGGAATCAGAATCAAGTCTCTCATGGATCGG 1189
 Db 841 GTTGGCAAGCAGCGGCCCAAGCTGTGACAGAGGAATGGAGAACTAATGGAAGCAG 900
 QY 1190 CTGATATGCAACAGTGTGTACATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACA 1249
 Db 901 CTGACGCTGACGGCAACGGTTAATTGACTACGAGCAATTCGTCACCGCAACAGTGCATA 960
 QY 1250 TGAACAAGATGAGAGAGAGAGATTTGTTGGTGTGCTGCTTTTGGACTTTGACAAAGACG 1309
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 QY 1370 ATACACCT---CTGAGCAGCATGATCAAGAGATTTGATCTTTGACAATGACGGGAAGTCG 1426
 Db 1081 ACGCGGATAAAATCAAGACATCATCTCCGATGCCGACTCTGACAATGATGGAAGGATAG 1140
 QY 1427 ATTTCTCGAGTTTACAGCAATGATGAGGAAGGAGATGAGTGTGGAGAGAGAGACCA 1486
 Db 1141 ATATTTCAGAGTTTGTGGGATGATGAGGAAGGAGCGGTGTCGCCGAGCAATGAACA 1200
 QY 1487 TGATGAAGA 1495
 Db 1201 TCAAGAAGA 1209

RESULT 3
 US-08-459-595A-20
 Sequence 20, Application US/08459595A
 Patent No. 6018104
 GENERAL INFORMATION:
 APPLICANT: Kosziel, Michael G.
 APPLICANT: Desai, Nalini M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Launis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6018104artis Corporation
 STREET: Patent & Trademark Dept., 520 White Plains
 STREET: Rd., POB 2005

Mon Mar 31 13:53:42 2003

CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
NAME: Pace, Gary M.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/Cip/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for n
OTHER INFORMATION: pollen-specific calcium dep
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-595A-20

Query Match	24.6%;	Score 429.8;	DB 3;	Length 1349;
Best Local Similarity	60.3%;	Pred. No. 1.4e-99;		
Matches	729;	Conservative 0;	Mismatches 477;	Indels 3; Gaps
QY	290	TTGAGATCATGATCATCTCTGAGCATCCAAATGTTGTTAGGATCAAGAGCACTTATG	349	
Db	1	TGAGATCATGATCACCACTCTCGGCCACCCACAGTGTGGCCCTCGCGCGCGGTACG	60	
QY	350	AAGATTGGGTGTTTTCATATTGTTATGAGAGGTTTGTGAAGTGGTGAGCTTTTGTATC	409	
Db	61	AGGACAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGCGCGGCGGGAGCTCTTTCGACC	120	
QY	410	GGATTGTTCTAAGGTGCTATTTAGTGTAGCGGTGAAGCTGTCAAGCTTATTAAGACGATTTC	469	
Db	121	GCATCATCGCCCGGGGCGAGTACAGGAGCGGCGGCCCGGAGCTGCTGCGCCGCATCG	180	
QY	470	TTGGTGTGTTTGAGGCTTGTCATCTCTCTGGTGTATTAGCATAGAGATCTCAAACTCGAGA	529	
Db	181	TGCAGATCGTGCAACCTGCCACTCCATCGGCGGTGATGCACCGGGACATCAAGCCCGAGA	240	
QY	530	ATTTCTTTGTTGTATAGHCCTAAAGATGATGCTAAGCTTAAGCTACCGATTTGTGTTCT	589	
Db	241	ACTTCTCTGCTCTCAGCAAGGACGAGGACGCGCGCTCAAGGCCACCGACTCTCGGCCCT	300	
QY	590	CTGCTCTTCTATAAGCCAGGACAATATTTATATCAGCTAGTTGGAAGTCGGTACTATGTTG	649	
Db	301	CCGTCTCTTCAAGGAGGCGGAGCTGCTCAGGACATCGTCGSCAGCGCTACTACATCG	360	
QY	650	CACGAGAGGTGCTAAAGAAATGTTATGGACCTGAATAGATGTGTGAGTGTCTGGTGTTA	709	
Db	351	CGCCCGAGGTGCTCAAGAGGAAGTACGCGCGGAGGCGGCACATCTGAGCGTCCGGCTCA	420	

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RESULT 4
US-08-459-504B-20
; Sequence 20, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lytle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.

```

APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 3..1226 /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."

US-08-459-504B-20

Query Match 24.6%; Score 429.8; DB 3; Length 1349;
Best Local Similarity 60.3%; Pred.No.1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
QY 290 TTCAGATATGCAATCATCTCTGAGCATCCAAATGTTGTAGGATCAAGGGACTTATG 349
DB 1 TGCAGATATGCAATCATCTCTGAGCATCCAAATGTTGTAGGATCAAGGGACTTATG 60
QY 350 AAGATTCGGTGTGTTTCATATGTTATGAGGTTTGTGAAGTGTGTGAGCTTTTGTATC 409
DB 61 AGGCAAGCAGACGCGTGCACCTCTGTCATGAGCTGTGCGCGCGGGAGCTCTTCGACC 120
QY 410 GGATGTTTCTAAAGTTCATTTTAGTGAGCGTCAAGCTGTCAAGCTTATTAAGCAATTC 469
DB 121 GCATCATCGCCGGGCCAGTACACGAGCGCGCGCGGAGCTGCTCGCGCCATCG 180
QY 470 TTGGTGTGTTGAGGCTTGTCTATCTCTTGGTGTATGATGATAGAGATCTCAAACCTGAGA 529

DB 181 TGCAGATCGTGCAACACTGCCACTCCATGGGGTGTATGCAACCGGACATCAAGCCGAGA 240
QY 530 ATTTCCTTGTGTTAGTAGTCCCTAAAGATGATGCTAAGGCTTAAGGCTTACCGATTTGTTGT 589
DB 241 ACTTCCTGCTCTCAGCAAGACAGGACGCGCGCTCAAGGCCACCGACTTCGGCCCTCT 300
QY 590 CTGCTCTTATAAGCCAGGACAATATTATATGACGTAGTTGGAAGTCCCTACTATCTTGT 649
DB 301 CCGTCTTTTCAAGGAGGCGAGCTGCTCAGGGACATCGTCGGCAGCGCCTACTACATCG 360
QY 650 CACCAGAGTGTCTAAAGAAATGTTATGACCTGAAATAGATGTGTGAGTGTGTTGTTA 709
DB 361 CGCCGAGGTGCTCAAGAGGAAGTACGCGCGCGGAGCGACATCTGGAGGCTCGGCTCA 420
QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTCCCTTCTGGGAGAGACTGAGTCTGGAATCT 769
DB 421 TGCTCTACATCTTCTCGCGCGGTGCTCTCCCTTCTGGGAGAGACAAGACGGCACT 480
QY 770 TTACAGAGATTTGCAAGGAAGTTAGATTTCAAATCTGACCCGTGCGCTTACTCTCAG 829
DB 481 TCACCGCATCTCGGAGGCGAGCTTGACCTCTCCAGCGAGCCATGCCACACATCTCGC 540
QY 830 AAGCTGCTAAGATTGATCTATAAATGCTCGAAGAGAGCCCCCAAGAACGATTTCTG 889
DB 541 CGGAGCGCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGCTCAC 600
QY 890 CTCATGAAGCCTTGTGTACCCATGGATTCTCGATGAACAAGCAGCAGCAGCAAGCGCTC 949
DB 601 CGTTCAGGTCTCAATCACCCTGATCAAGAAGACGAGAGCGCGCTTGACACGCGC 660
QY 950 TTGATCCAGCAGCTTATCTCGTCTAAAGCAGTTTCTCAATGAATTAAGATTAAGAAA 1009
DB 661 TTGACAACGTTGTTCTGCACAGGCTCAAGCAGTTTCAGGGCCATGAACCACTTCAAGA 720
QY 1010 TGGCATTCGGGTAATTCGTGAGAGACTTTCAGAGGAGAAATTTGGAGTCTGAAGAA 1069
DB 721 CAGCATTTGAGGATCATAGCTGGGTGGCTATCCGAAGAGGAGATCACAGGCTGAAG 780
QY 1070 TGTTCAGATGATAGACACAGACAACAGCGGAACGATTCTTTTGAAGACTCAAGCGG 1129
DB 781 TGTTCAGAACATGACAGAGATACAGCGGGACCATTACCTCTCGAGAGCTCAACACG 840
QY 1130 GTTTGAAGAGTGGGATCTGAATGGAATCAAGAAATCAAGTCTCTCATGATGCGG 1189
DB 841 GSTTGCACAGCAGCGGCGCCCAAGCTGTACAGACAGCGAAATGGAGAACTAATGGA 900
QY 1190 CTGATATCGACAACAGTGTGTACATAGACTACGAGAAATTCCTAGCAGCAACCTTACA 1249
DB 901 CTGACGCTGACGCGACGGTTAATTGACTTACGACGAATTCGTCAACGCAACAGTGA 960
QY 1250 TGAACAAGATGGAGAGAGAGATCTGTGGTGTGCTATTTCGACTTTGACAAAGACG 1309
DB 961 TGAACAACCTGGATAGAGAAGACCACTTTACACAGCATTCAGTATTCGACAGGACA 1020
QY 1310 GAAGCGTTATATCACCATCGATGAGCTTCAGTCACTGTGACAGAGATTTGGTCTATG 1369
DB 1021 ACAGCGGTGATACATTACTAAGAAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGTTCT 1080
QY 1370 ATACACT--CTGGACGACATGATCAAGGAGATTGATCTTGACATGACGGAGATCG 1426
DB 1081 ACCCGGATAAATCAAGACATCATCTCCGATGCCACTCTGACATGATGAAGAGATAG 1140
QY 1427 ATTTCTCGAGTTTACAGCAATGATGAGGAAGGAGATGGAGTTGGGAGAGCAGAACCA 1486
DB 1141 ATTATTACAGTTTGTGGGATGATGAGGAAGGAGGAGCTGTTGCTGCGGACCAATGA 1200
QY 1487 TGATGAAGA 1495
DB 1201 TCAAGAAGA 1209
RESULT 5

US-08-459-444-20

Sequence 0, Application US/08459444A

Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lytle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/PI/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note- "cdna sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-08-459-444-20

Query Match 24.6%; Score 429.8; DB 3; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

QY 290 TTCAGATCATGTCATCTCTGAGCATCCAAATCTTGTAGGATCAAGGGACTTANG 349

Db 1 TGCAGATCATGACCACCTCTCCGGCCAGCCCACTGTGGCCCTCCCGCGCGCTACG 60

QY 350 AAGATTCGGTGTGTTGTCATATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTATC 409

Db 61 AGGAAAGAGAGAGCGTGCACCTCGTCATGAGCTGTCCGCGCGGAGCTCTTCGAC 120

QY 410 GGATTTGTTCTTAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAAGACGATTC 469

Db 121 GCATCATCGCCCGCGCCAGTACACGAGCGCGCGCGGAGCTGCTCGCGGCCATCG 180

QY 470 TTGGTGTGTTGAGGGTGTGTCATCTCTGGTGTATGATAGATGATCTCAACCTGAGA 529

Db 181 TGCAGATCGTGCACACTGCCCTCCATGGGGGTGATGACCGGGACATCAAGCCCGAGA 240

QY 530 ATTTCTTTTIGATAGTCTTAAAGATGATGCTAAAGCTTAAGCTACCGATTTTGGTTTGT 589

Db 241 ACTTCTGTGCTCAGCAAGGACGAGGACGCGCGCTCAGGCCCACCGACTTCGGGCTCT 300

QY 590 CTGCTTCTATAAGCCAGGACATATTTATGACGTAGTTGGAAGTCCGCTACTATGTTG 649

Db 301 CGCTCTTCTTCAAGGAGGCGGAGCTGCTCAGGGACATCTCGCAGCGGCTACTACATCG 360

QY 650 CACCAGAGGTGCTAAAGAAATGTATGGACCTGAATATAGATGTGTGGAGTGTGGTGTGA 709

Db 361 CGCCCGAGGTGCTCAGAGGAGAGTACGGCCGAGGCGGCACATCTGGAGCGTCGGGTCA 420

QY 710 TCCTCTACATTTTACTCAGCGGTGTTCCCTCCCTTCTGGGCGAGAGTGTGATCTGGAATCT 769

Db 421 TGCTCTACATCTTCCCTCGCGCGGTGCTCCCTTCTGGGCGAGAGAACGAGACGGCATCT 480

QY 770 TTAGACAGATATTGCAAGGAGGAGTTAGATTTCAAATCTGACCCGTGCGCTACTATCTCAG 829

Db 481 TCACCCGCATCTCGGAGGCGCAGCTTGACCTCTCCAGCGAGCCATGCCACATCTCGC 540

QY 830 AAGCTGCTTAAAGATTGATCTATAAATGCTCGAAAGGAGGCCCCCAAGAACGCAATTTCTG 889

Db 541 CGGGAGCCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGCTCACCG 600

QY 890 CTCATGAAGCCTTGTCTCACCCTGATGATGTCATCAACCAAGCAGCACAGCAAGCCCTC 949

Db 601 CGTTCAGGTCCTCAATCACCCATGGATCAAGAGACGAGCGCGCTGACACCCGCG 660

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QY 1070 TGTTCAGATGTAGACACAGCAACAGCGGAGCTTACTTTTGAAGAGCTCAAGCGG 1129

Db 781 TGTTCAAGACATGACAGAGGATACAGCGGGACCAATTCCTCGACGAGCTCAAAACG 840

QY 1130 GTTTGAAGAGAGTCGGATCTGAATGGAATCAAGAAATCAAGTCTCTCATGGATCGCG 1189

Db 841 GGTTCGCAAGCAGCGGCGCCCAAGCTGTACAGACAGCGGAATGAGAACTAATGGAAGCAG 900

QY 1190 CTGATATCGACACAGTGTGTACAAATAGACTACGGAGAAATCTAGCAGCAACCTTACACA 1249

Db 901 CTGACCTGACGGCAACGGGTAAATTTACTACGAGAAATTCGTCAACCCTCAACAGTGCATA 960

QY 1250 TGAACAAGATGGAGAGAGGAGATTTCTGGTGGCTGCATTTTCGGACTTTTGACAAAGAGC 1309

Db 961 TGAACAACCTGGATAGAGAGGACACCTTTACACAGCATTCACGATTTTCGACAAAGGACA 1020

QY 1310 GAAGCGGTTATATFACCATCGATGAGCTTCAGTCAAGTTCAGCAGAGTTTGGTCTATGTC 1369

Db 1021 ACAGCGGGTACATTTACTTAAAGAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGGTGTATG 1080

QY 1370 ATACACCT---CTGGACGACATGATCAAGGAGATTGATCTTACAAATGACGGGAGAGTCG 1426

Db 1081 AGCCGATTAATAATCAAGAGACATCTCCGATGCCGACTCTGCATATGATGGAAGGATAG 1140

QY 1427 ATTTCTCGGAGTTTACGCAATGATGAGGAAAGAGATGGAGTTGGGAGAACGACCAACA 1486

Db 1141 ATTATTCAGAGTTTGTGGCGATGATGAGGAAAGGAGCGCTGGTCCCGAGCCCATGAACA 1200

QY 1487 TGATGAAGA 1495

Db 1201 TCAGAGAGA 1209
| | | | |
1 TCGAGATCATGACACACCTCTCCGGCCAGCCCAAGCTGGTGGGCTCCGCGCGGTACG 60
QY 350 AAGATTCGGTGTTCATATTTGTTAGAGGTGTGAAAGGTGGTGGTGTGATC 409
| | | | |
Db 61 AGGACAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGCGCGGGGGAGCTCTTCGACC 120
QY 410 GGATTTTTCCTAAGGTTCATTTAGTGAGCGTGAAGCTGTCAAGCTTTATTAAAGAGATTC 469
| | | | |
Db 121 GCATCATGCGCGCGGGCCAGTACAGGAGCGCGCGCGGAGCTGTGCGCGGCATCG 180
QY 470 TTGGTGTGTTGAGCGTGTCTCTTCTGTTGTTATGATCATAGAGATCTCAACCTGAGA 529
| | | | |
Db 181 TGCAGATCGTGCACACCTGCCACTCCATGGGGGTGATCACCGGAGACATCAAGCCCGAGA 240
QY 530 ATTTCTGTTTGTATAGTCTCTAAGATGATGCTAAAGCTTAAGCTTAAGCTTAAAGCTTGGTTGT 589
| | | | |
Db 241 ACTTCTGCTGCTCAGCAAGCAGGAGCGCGCTCAAGGCCACCGACTTCGSCCTCT 300
QY 590 CTGCTCTCTATAAGCCAGGACAATATTTATGACGTAGTTGGAAGTCGGTACTGTTG 649
| | | | |
Db 301 CCGTCTTCTTCAAGGAGGCGAGCTGCTCAGGACATCGTCGGCAGCGCTACTACATCG 360
QY 650 CACCAGAGTGTCTAAGAAATGTTATGACCTGAATAGATGTGTGGAGTCTGTTGTTA 709
| | | | |
Db 361 CGCCGAGGTGCTCAAGAGGAGTACGCGCGGAGGCGGACATCTGGAGCGTCGCGCTCA 420
QY 710 TCCTCTACATTTACTCAGCGGTGTTCTCTCTGGCAGAGACTGAGTCTGGAATCT 769
| | | | |
Db 421 TGTCTACATCTCTCTCGCGCGTGCCTCTCTCTGGCAGAGAACGAGACGCACT 480
QY 770 TTAGACAGATATGCAAGGAGTGTAGATTTCAAAATGACCCCGTGGCTACTACTCTCAG 829
| | | | |
Db 481 TCACCGCATCTCTCGAGGCGAGCTTGACCTCTCCAGGAGCGCATGGCAGCATCTCGC 540
QY 830 AAGCTGCTAAGATTTGATCTATAAATGCTCGAAGAGCGCCCAAGAACGCACTTTCTG 889
| | | | |
Db 541 CGGAGCCAGGATCTCTCAAGAAATGCTCAACATCAACCCCAAGGAGCGCTCAGG 600
QY 890 CTCATGAAGCCTTGCTCAGCAGCTTTGTCGATGAAGAACAGCAGCAGCAGCAGCCTC 949
| | | | |
Db 601 CGTTCAGGTCTCTCAATCACCCTGATGATCAAGAGAGCGAGCGCTGACAGCGCGC 660
QY 950 TTGATCCAGAGTCTTATCTCGTCAAGAGAGTTTCTCAATGATGATGATGATGATG 1009
| | | | |
Db 661 TTGACACGCTTGTCTCGACAGGCTCAAGCAGTTCAGGCGCATGAACAGTTCAGAAAG 720
QY 1010 TGGCATTACGGGTAACTGCTGAGAGACTTTTCAGAGAGAAATTCGAGGTCTGAAGGAT 1069
| | | | |
Db 721 CAGCATTCAGGATCATAGCTGGTGGCTTATCGAAGAGAGATCAGAGGCTGAAGGAGA 780
QY 1070 TGTTCAGATGATAGACAGACAGCAGCGGAGATTTCTTTTGAAGAGCTCAAGCGG 1129
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Db 781 TGTTCAGAGATTCAGAGGATTAACAGCGGACCTTACCTCGACAGCTCAACACG 840
QY 1130 GTTTCAGAGAGTCCGATCTGACTGATGATCAGAAATCAAGTCTCATGATGATGCGG 1189
| | | | |
Db 841 GGTTCGAAAGCAGCGGCGGCTGATGATCAGACAGGAAATGGAGAAATTAATGGAAGCAG 900
QY 1190 CTGATATCGACAACAGTGTGTACATAGACTACGGAGATTTCTAGCAGCAGCTTACACA 1249
| | | | |
Db 901 CTGAGCTGACGGCAACGGGTTAATGACTAGGAGATTCGTCAACCCACAGTGCATA 960
QY 1250 TGACAAGATGGAGAGAGAGATTTGTTGGTGTGATTTTTCGAGCTTTGACAAGAGC 1309
| | | | |
Db 961 TCACAAATCTGATAGAGAGAGCAGCTTTACACAGCATTCAGATTTTCGACAAAGGACA 1020
QY 1310 GAAGCGGTATATCACCATCGATGAGCTTCAGTTCAGCTTGACAGAGTTTGTCTATGTG 1369
| | | | |
Db 1021 ACAGCGGTATATCTACTAAGAGAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGGTGTATG 1080
QY 1370 ATACACCTT---CTGACCGACATGATCAAGGAGATTTGATCTTGAACAATCAGGGAGATCG 1426
| | | | |

Db 1201 TCAGAGAGA 1209
| | | | |
1 TCGAGATCATGACACACCTCTCCGGCCAGCCCAAGCTGGTGGGCTCCGCGCGGTACG 60
QY 350 AAGATTCGGTGTTCATATTTGTTAGAGGTGTGAAAGGTGGTGGTGTGATC 409
| | | | |
Db 61 AGGACAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGCGCGGGGGAGCTCTTCGACC 120
QY 410 GGATTTTTCCTAAGGTTCATTTAGTGAGCGTGAAGCTGTCAAGCTTTATTAAAGAGATTC 469
| | | | |
Db 121 GCATCATGCGCGCGGGCCAGTACAGGAGCGCGCGGAGCTGTGCGCGGCATCG 180
QY 470 TTGGTGTGTTGAGCGTGTCTCTTCTGTTGTTATGATCATAGAGATCTCAACCTGAGA 529
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Db 181 TGCAGATCGTGCACACCTGCCACTCCATGGGGGTGATCACCGGAGACATCAAGCCCGAGA 240
QY 530 ATTTCTGTTTGTATAGTCTCTAAGATGATGCTAAAGCTTAAGCTTAAAGCTTGGTTGT 589
| | | | |
Db 241 ACTTCTGCTGCTCAGCAAGCAGGAGCGCGCTCAAGGCCACCGACTTCGSCCTCT 300
QY 590 CTGCTCTCTATAAGCCAGGACAATATTTATGACGTAGTTGGAAGTCGGTACTGTTG 649
| | | | |
Db 301 CCGTCTTCTTCAAGGAGGCGAGCTGCTCAGGACATCGTCGGCAGCGCTACTACATCG 360
QY 650 CACCAGAGTGTCTAAGAAATGTTATGACCTGAATAGATGTGTGGAGTCTGTTGTTA 709
| | | | |
Db 361 CGCCGAGGTGCTCAAGAGGAGTACGCGCGGAGGCGGACATCTGGAGCGTCGCGCTCA 420
QY 710 TCCTCTACATTTACTCAGCGGTGTTCTCTCTGGCAGAGACTGAGTCTGGAATCT 769
| | | | |
Db 421 TGTCTACATCTCTCTCGCGCGTGCCTCTCTCTGGCAGAGAACGAGACGCACT 480
QY 770 TTAGACAGATATGCAAGGAGTGTAGATTTCAAAATGACCCCGTGGCTACTACTCTCAG 829
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Db 481 TCACCGCATCTCTCGAGGCGAGCTTGACCTCTCCAGGAGCGCATGGCAGCATCTCGC 540
QY 830 AAGCTGCTAAGATTTGATCTATAAATGCTCGAAGAGCGCCCAAGAACGCACTTTCTG 889
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Db 541 CGGAGCCAGGATCTCTCAAGAAATGCTCAACATCAACCCCAAGGAGCGCTCAGG 600
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Db 601 CGTTCAGGTCTCTCAATCACCCTGATGATCAAGAGAGCGAGCGCTGACAGCGCGC 660
QY 950 TTGATCCAGAGTCTTATCTCGTCAAGAGAGTTTCTCAATGATGATGATGATGATG 1009
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Db 661 TTGACACGCTTGTCTCGACAGGCTCAAGCAGTTCAGGCGCATGAACAGTTCAGAAAG 720
QY 1010 TGGCATTACGGGTAACTGCTGAGAGACTTTTCAGAGAGAAATTCGAGGTCTGAAGGAT 1069
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Db 721 CAGCATTCAGGATCATAGCTGGTGGCTTATCGAAGAGAGATCAGAGGCTGAAGGAGA 780
QY 1070 TGTTCAGATGATAGACAGACAGCAGCGGAGATTTCTTTTGAAGAGCTCAAGCGG 1129
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Db 781 TGTTCAGAGATTCAGAGGATTAACAGCGGACCTTACCTCGACAGCTCAACACG 840
QY 1130 GTTTCAGAGAGTCCGATCTGACTGATGATCAGAAATCAAGTCTCATGATGATGCGG 1189
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Db 841 GGTTCGAAAGCAGCGGCGGCTGATGATCAGACAGGAAATGGAGAAATTAATGGAAGCAG 900
QY 1190 CTGATATCGACAACAGTGTGTACATAGACTACGGAGATTTCTAGCAGCAGCTTACACA 1249
| | | | |
Db 901 CTGAGCTGACGGCAACGGGTTAATGACTAGGAGATTCGTCAACCCACAGTGCATA 960
QY 1250 TGACAAGATGGAGAGAGAGATTTGTTGGTGTGATTTTTCGAGCTTTGACAAGAGC 1309
| | | | |
Db 961 TCACAAATCTGATAGAGAGAGCAGCTTTACACAGCATTCAGATTTTCGACAAAGGACA 1020
QY 1310 GAAGCGGTATATCACCATCGATGAGCTTCAGTTCAGCTTGACAGAGTTTGTCTATGTG 1369
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Db 1021 ACAGCGGTATATCTACTAAGAGAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGGTGTATG 1080
QY 1370 ATACACCTT---CTGACCGACATGATCAAGGAGATTTGATCTTGAACAATCAGGGAGATCG 1426
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US-09-547-422-20
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize
; pollen-specific calcium dependent protein kinase gene as
; disclosed in Figure 30."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1226
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-547-422-20
Query Match 24.6%; Score 429.8; DB 4; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
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Db 1081 AGCGGATAAATCAAGACATCACTCCGATGCGGACTCTGACAAATGATGAAGGATAG 1140
QY 1427 ATTTCGCGATTACAGCAATGATGAGAAAGGAGATGGAGTTGGGAGAAGCAGAACCA 1486
Db 1141 ATTATTCAGAGTTTGCGCGATGATGAGAAAGGACGCGTGGTCCGAGCCATGAACA 1200
QY 1487 TGATCAAGA 1495
Db 1201 TCAAGAGA 1209

RESULT 7
US-08-459-448A-26
; Sequence 26 Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
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LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-448A-26
Query Match 12.5%; Score 218; DB 2; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 142 TACCTTCTGGGAAAAAGCTAGGCCAAATTTGGAAACAACCTATCTCTGCACAGAG 201
Db 1757 TACTCGATGGCAAGGAGCTCGGCGCGGCGGCTGCGGTGACGACCTGTGCACGCAC 1816
QY 202 AATATCAACCTCCGCTAATTACGCTCAATATCCGGAAGGAAAGCTGTGTGTGTCGC 261
Db 1817 CGGACGAGGCGGCGAGAAGCTGGCGTCAAGACGATCGGGAAGCGGAGCTGGCGCCAGG 1876
QY 262 GAGGATTACGAGATGATGGCTGAGATTCAGATCATCATCATCTCTCTGAGCATCA 321
Db 1877 GAGGACGTGACGACCTGCGGGGAGGTGACATCATCATCTCTCCGCCAGGCC 1936
QY 322 AATGTTTGTAGGATCAAGGGGACTTATGAAGATTCGCTGTTTGTTCATATTTGTTAGG 381
Db 1937 AAGTGTGTGGCTCCGCGGCGGTACGAGGACAAACGAGCGGTGCACCTCTGTCATGGAG 1996
QY 382 GTTTGTGAAGGCTGCTGAGCTTTTGTGATCGGATTTTCTTAAAGGTCATTTTGTAGCGCT 441

Db 1997 CTGTGCGGGGGGAGCTTTTCGACCGCATCATCGCCGGGGCCAGTACACGGAGCGC 2056
QY 442 GAAGCTCTCAAGCTTATTAAGACGATTCCTGGTGTCTTGTAGGCTTGTCTATCTCTTGGT 501
Db 2057 GGCCTCGGAGGCTGTGCGGGCCATCGTGCAGATCGTGCACACTGCCACTCCATGGGG 2116
QY 502 GTTATGATAGAGATCTCAACACCTGAGAAATTCCTTTGATAGTCTCTAAAGATGATGCT 561
Db 2117 GTGATGACCGGACATCAAGCCCGGAGAACTTCCTGTGCTCGACAGGAGGAGGAGCGC 2176
QY 562 AAGCTTAAGGCTACCGATTTTGTCTGTCTCTCTATAGCCAGGACATATTTATAT 621
Db 2177 CCGCTCAAGGCCACCGCTTCGGGCTCTCGGCTCTCTCTCAAGGAGGCGAGCTCTCAGG 2236
QY 622 GACGTAGTTGGAAGTCGCTACTATGTGACCCAGAGGTGCTAAAGAAATGTTATGGACCT 681
Db 2237 GACATCGTCGCGAGCGCTACTATCATCGCCCGAGGTGCTCAAGAGAAAGTACGGCCG 2296
QY 682 GAATAGATGTGGATGCTGTGGTGTATCTCTACATTTTACTCAGCGGTGTTCTCTCC 741
Db 2297 GAGCCGACATCTGAGCGGTGGGGTCTATGCTCTACATCTCTCTCGCGGGGTCTCTCC 2356
QY 742 TTCGGGCGAG 751
Db 2357 TTCGGGCGAG 2366

RESULT 8

US-08-459-595A-26
Sequence 26, Application US/08459595A

Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,595A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
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NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL

US-08-459-595A-26

Query Match

Best Local Similarity 12.5%; Score 218; DB 3; Length 4162;

Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

142	QY	TACCTTCTGGGAAAAGCTAGCCAGGCCAAATTGGAACAACCTATCTCTGCACAGAG	201
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202	QY	AAATCAACCTCCGCTAAATTACGCTGCAATCGATCCCGAAGCGAAAGCTCGTGTGCGC	261
1817	Db	CGGACGCGGGCGAGAGCTGGGTGCAAGACGATCGGAAGCGGAAGCTGGCGGCCGAGG	1876
262	QY	GAGGATTACGAAGATGATGGCTGAGATTCAGATCATCATCATCTCTTGAGCATCCCA	321
1877	Db	GAGGAGCTGGACACGCTCGCGCGGGAGGTGCAGATCATGCAACCACTCTCCGCGCCAGCCC	1936
322	QY	AATGTGCTTAGGATCAAGGGACTTATGAAGATCGGTGTTTGTTCATATTGTTATGGAG	381
1937	Db	AAGTGGTGGGCGCTCGCGGCGCGTACGAGGACAAAGCAGACGCTGCACCTCGTCATGGAG	1996
382	QY	GTTTGTCAAGGTGGTGAGCTTTTGTATCGGATGTGTTCTAAAGGTCACTTTTAGTGAGCGT	441
1997	Db	CTGTGCGGGCGGGAGCTCTTCGACCGCATCATCGCCCGGGGCCAGTACACGGAGCGC	2056
442	QY	GAAGCTGTCAAGCTTATTAAGACGATCTWTGGTGTGTTGAGGCTGTCATCTCTTGGT	501
2057	Db	GGCGCCGCGGAGCTGTGCGCGCCATCTGTGCAGATCGTCACACTGCCACTCCATGGGG	2116
502	QY	GTATGTCATGAGATCTCAAACTGAGAAATTTCTGTTTGATAGTCCCTAAAGATGATGCT	561
2117	Db	GTATGTCACGGGACATCAAGCCGAGAACTTCTGCTGCTCAGCAAGGACGAGAGCGG	2176
562	QY	AAGCTTAAGCTACCGATTTTGGTTGTGCTGTCTCTATAAGCCAGGACAATATTTATAT	621
2177	Db	CCGCTCAAGGCCACCGACTCGGCTCTCCGCTCTTCTCAAGGAGGGGAGCTGCTCAGG	2236
622	QY	GAGCTAGTGGAGTCGGTACTATGTTGCACAGAGGTGCTTAAGAAATGTTATGGACCT	681
2237	Db	GACATCGTGGCAGGCGCTACTACATCGCGCGCGAGGTGCTCAAGAGGAAGTACGGCCG	2296
682	QY	GAATAGATGTGGAGTGCTGGTGTATTCCTACATTTTACTCAGCGGTGTTCTCTCCC	741
2297	Db	GAGGCCACATCTGGAGGCTCGGCTCATGCTCATATCTTCTCGCGGGCGTGGCTTCCC	2356
742	QY	TTCTGGGCGAG	751
2357	Db	TTCTGGGCGAG	2366

RESULT 9

US-08-459-504B-26
; Sequence 26, Application US/08459504B

Patent No. 6075185

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: GENERAL INFORMATION:
:
: APPLICANT: Koziel, Michael G.
: APPLICANT: Desai, Nalini M.
: APPLICANT: Lewis, Kelly S.
: APPLICANT: Kramer, Vance C.
: APPLICANT: Warren, Gregory W.
: APPLICANT: Evola, Stephen V.
: APPLICANT: Crossland, Lydie D.
: APPLICANT: Wright, Martha S.
: APPLICANT: Merlin, Ellis J.
: APPLICANT: Launis, Karen L.
: APPLICANT: Rothstein, Steven J.
: APPLICANT: Bowman, Cindy G.
: APPLICANT: Dawson, John L.
: APPLICANT: Dunder, Erik M.
: APPLICANT: Pace, Gary M.
: APPLICANT: Suttie, Janet L.
: TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
: TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
: NUMBER OF SEQUENCES: 94

```

ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park

```

1  STATE:  NC
2  COUNTRY:  USA
3  ZIP:  27709
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE:  Floppy disk
6  COMPUTER:  IBM PC compatible
7  OPERATING SYSTEM:  PC-DOS/MS-DOS
8  SOFTWARE:  PatentIn Release #1.0, Version #1.30
9  CURRENT APPLICATION DATA:
10 APPLICATION NUMBER:  US/08/459,504B
11 FILING DATE:
12 CLASSIFICATION:
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER:  US 08/459,595
15 FILING DATE:  02-JUN-1995
16 APPLICATION NUMBER:  US 07/951,715
17 FILING DATE:  25-SEP-1992
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER:  US 07/772,027
20 FILING DATE:  04-OCT-1991
21 ATTORNEY/AGENT INFORMATION:
22 NAME:  Meigs, J. Timothy
23 REGISTRATION NUMBER:  38,241
24 REFERENCE/DOCKET NUMBER:  CGC1577/CIP/DIV
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE:  (919)541-8587
27 TELEFAX:  (919)541-8689
28 INFORMATION FOR SEQ ID NO: 26:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH:  4162 base pairs
31 TYPE:  nucleic acid
32 STRANDEDNESS:  single
33 TOPOLOGY:  linear
34 MOLECULE TYPE:  DNA (genomic)
35 HYPOTHETICAL:  NO
36 FEATURE:
37 NAME/KEY:  misc_feature
38 LOCATION:  1418..1427
39 OTHER INFORMATION:  /note= "start of mRNA"
40 FEATURE:
41 NAME/KEY:  exon
42 LOCATION:  1481..2366
43 FEATURE:
44 NAME/KEY:  intron
45 LOCATION:  2367..2451
46 FEATURE:
47 NAME/KEY:  exon
48 LOCATION:  2452..2602
49 FEATURE:
50 NAME/KEY:  intron
51 LOCATION:  2603..2690
52 FEATURE:
53 NAME/KEY:  exon
54 LOCATION:  2691..2804
55 FEATURE:
56 NAME/KEY:  intron
57 LOCATION:  2805..2906
58 FEATURE:
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63 LOCATION:  3076..3177
64 FEATURE:
65 NAME/KEY:  exon
66 LOCATION:  3178..3304
67 FEATURE:
68 NAME/KEY:  intron
69 LOCATION:  3305..3398
70 FEATURE:
71 NAME/KEY:  exon
72 LOCATION:  3399..3498
73 FEATURE:

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NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
US-08-459-504B-26

Query Match 12.5%; Score 218; DB 3; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 142 TACCTTCGGAAGAAAGCTAGGCGCAATTTGGAACAACCTATCTCTGCACAG 201
Db 1757 TACTCGATGGCAGAGGAGCTCGGGCGGCGAGTTGCGCGTGCACCTGTGCACGAC 1816
QY 202 AAATCAACCTCCGTAAATAGCCCTGCAATCGATCCCGAAGCAAGCTCGTGTGCGC 261
Db 1817 CGGACGAGCGCGAGAGCTGGCGTGAAGACGATCGCGAAGCGAAGCTGCGCGCCAGG 1876
QY 262 GAGGATTACGAGATGATGCGCTGAGATTCAGATCATGATCATCTCTCTGAGCATCCA 321
Db 1877 GAGGACGTGGACGAGTGGCGCGGAGGTGCAGATCATGACCACTCTCGCGGCAGGCC 1936
QY 322 AATGTTGTAGGATCAAGAGACCTTATGAAGATTCGGTGTGTTGTTTCATATTGTTATGAG 381
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Db 2057 GCGCGCGGAGCTGCTCGCGGCGCATGTCGAGATCTGTGACACCTGCGCATCTCCATGGG 2116
QY 502 GTTATGATAGATCTCAACCTGAGATTTCTTGTGTTGATAGTCTTAAAGATGATGCT 561
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Db 2177 CCGCTCAAGCCCGGAGCTCTCGGCGCTCTCTCTCTCTCTCAAGGAGGCGGAGCTCTCAGG 2236
QY 622 GAGTATGAGTCCGCTACTATGTTGACAGAGTGTCTAAAGAAATGTTATGACCT 681
Db 2237 GACATCTCGCAGCGCTACTATCTGCTGCGCGGAGTGTCTAAGAGAGTACGCGCGG 2296
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Db 2357 TTCTGGGCGAG 2366

RESULT 10
US-08-459-444-26
Sequence 26, Application US/084594444
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: KozieL, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Launis, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/GC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
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LOCATION: 3178..3304
FEATURE:
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LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon

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FEATURE: intron
NAME/KEY: 3499..3713
FEATURE: exon
NAME/KEY: 3714..3811
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-08-459-444-26

Query Match 12.5%; Score 218; DB 3; Length 4162;

Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 142 TACCCTCTGGGAAAAGTAGCCCAAGCCCAATTGGGAACACACCTATCTCTGCACAGAG 201
DB 1757 TACTCATGGGAAAGAGCTGGCGGGGAGTTCGGCGGTGACCGACCTGTGCACGCAC 1816
QY 202 AATCAACCTCGCTAATACGCTCAAAATGATCCCGAAGCAAGCTCGTGTGTGCTGC 261
DB 1817 CGGACGAGCGCGAGAGAGCTGGCTGCAAGACGATCGCGAGGAGTGGCGGCCAGG 1876
QY 262 GAGGATTAGAGATGATGCGGTGAGATTGAGATCATGATCATCTCTGAGCATCCA 321
DB 1877 GAGGAGCTGGAGCAGCTGGCGGGGAGGTCAGATCATGACACACCTCTCCGCCAGCCC 1936
QY 322 AATGTTGTTAGGATCAAAAGGAGCTATGAGATTCGGTGTGTTTCATATTTGATGGAG 381
DB 1937 AACGTTGGTGGCTCGCGCGGCTACGAGGACAGCAGCGTGCACCTCTGTCATGGAG 1996
QY 382 GTTGTGAAGGTGGTAGCTTTTGTATCGGATTTGTTCTAAAGGTCAATTTAGTACGCT 441
DB 1997 CTCTGCGCGGGGGAGCTCTCGACCGCATCATCGCCCGGGGCGAGTACACGGAGCGC 2056
QY 442 GAAGCTGCAAGCTTATTAAGAGATCTTGGTGTGTTGAGCTTGTCTATCTCTGTGT 501
DB 2057 GCGCGCGGAGCTGCTGCGCGCATCTGTCAGATGTCGACACCTGCCACTCCATGGGG 2116
QY 502 GTATGATAGATGATCTCAAACTGAGAAATTTCTTTGTATGATGCTCTAAAGATGATGCT 561
DB 2117 GTGATGACCGGACATCAAGCCCGAGAACTTCTGCTCTCAGCAGGACGAGGACGG 2176
QY 562 AAGCTTAAGCTAACGATTTTGGTGTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 621
DB 2177 CGGCTCAAGGCGACGACTGCGGCTCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCT 2236
QY 622 GAGCTAGTTGAAGTCCGCTACTATGTTGACACGAGGCTCTAAAGAAATGTTATGACCT 681
DB 2237 GACATGCTCGGACGCGCTACTACATCGCGCGGAGTCTCTCAAGAGGAGTACGCGCG 2296
QY 682 GAAATAGATGTTGAGTCTGCTGTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 741
DB 2297 GAGGCGGACATCTGAGGCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2356
QY 742 TTTCTGGGCGAG 751
DB 2357 TTTCTGGGCGAG 2366

RESULT 11

US-09-547-422-26
Sequence 26, Application US/09547422
Patent No. 6320100

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.

Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
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NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
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LOCATION: 2805..2906
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NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304

US-09-547-422-26

Query Match
Best Local Similarity 12.5%; Score 218; DB 4; Length 4162;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

YQ 142 TACCTTCTGGAAAAAGCTAGCCAAAGCCCAATTGGAAACACCTATCTCTGCACAG 201
DB 1757 TACTCGATGGCAAGAGCTCGCGCGCGGCGAGTTCGGCTGACGACCTGTGCAGCAC 1816
YQ 202 AAATCAACCTCCGCTAATTACGCTCAATCGATCCGAAACGAAAGCTGTGTGCGC 261
DB 1817 CGGACGAGCGCGAGAAGCTGGCGTCAAGACGATCGCAAGCGGAAGTGGCGGCCAGG 1876
YQ 262 GAGATTACGAAGATGATGGCTGAGATTCAGATCATCATCATCTCTGAGCATCCA 321
DB 1877 GAGGAGCTGGACGACCTGCGCGGGAGGTGCAGATCATGCACCACTCTCCGGCCAGGCC 1936
YQ 322 AATGTTGTTAGGATCAAAAGGACTTATGAAGATTCGGTCTGTTTTCATATTTATGGAG 381
DB 1937 AAGTGTGGGCTCCGCGCGCGTACGAGGACAACGAGCGTGCACCTGCTATGGAG 1996
YQ 382 GTTTGGAAGGTGGTGAGCTTTTGTGATTCGATTTTCTTAAGGTCATTTTATGAGCGT 441
DB 1997 CTGTGCGGCGGCGGAGCTCTTCGACCGCATATCGCCGCGGCGGCGAGTACACGAGCGC 2056
YQ 442 GAAGCTGCAAGCTTATTAAGACGATCTGTGGTGTGTTGAGCTTGTCTATCTCTTGT 501
DB 2057 GCGCGCGGAGCTGCTGCGCGCATCTGTCAGATCTGTCACACCTGCCACTCCATGGGG 2116
YQ 502 GTTATCATAGATCTCAAAACCTGAGAATTTCTGTTTATAGTCTCTAAAGATGATGT 561
DB 2117 GTGATGCAACCGGACATCAAGCCGAGAACTTCTGCTGTCAGCAAGGACGAGGACGGG 2176
YQ 562 AAGCTTAAGCTACCGATTTTGTGTTCTGCTCTTATTAAGCCAGGACAATTTATAT 621
DB 2177 CCGCTCAAGCCACCGACTTCGCGCTCTCTGCTCTTCAAGGAGGCGAGCTGCTCAGG 2236
YQ 622 GAGCTAGTTGAGTCCGCTACTATGTTGCAACGAGAGTGTCAAGAAATGTTATGAGACT 681
DB 2237 GACATGTCGCGACGCGCTACTACATGCGCGCGAGGTCTCAAGAGGAAGTACGCGCCG 2296
YQ 682 GAAATAGATGTGGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTCTCTCCC 741
DB 2297 GAGCCCGACATCTGAGGCTGCGCGCTATCTCTACATCTCTCTCCGCGGCTGCTCCC 2356
YQ 742 TTCTGGGCGAG 751
DB 2357 TTCGGGCGAG 2366

RESULT 12
US-07-951-715A-26
; Sequence 26, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.

LOCATION: 2907...3074
FEATURE:
NAME/KEY: intron
LOCATION: 3075...3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178...3305
FEATURE:
NAME/KEY: intron
LOCATION: 3306...3397
FEATURE:
NAME/KEY: exon
LOCATION: 3398...3497
FEATURE:
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NAME/KEY: exon
LOCATION: 3713...3811
US-09-951-715A-26

Query Match 12.5%; Score 218; DB 1; Length 4165;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 142 TACCTTCTGGGAAAGAACTAGGCAAGGCCAATTTGGAACAACCTATCTCTGCACAGAG 201
DB 1755 TACTCGATGGCAAGAGCTCGGCGGGCAGTTGCGCGGTGACGACCTGTGCACGCAC 1814
QY 202 AATCAACCTCCGCTAATTACGCTGCAATCGATCCGGAAGCAAGCTGCTGTGCGC 261
DB 1815 CGGACGAGCGGAGAGCTGGCGTGAAGACATCGCATCGGGAAGCAAGCTGCGGCGCAGG 1874
QY 262 GAGGATTACGAAGATGTATGCGCTGAGATTCAGATCATGATCATCTCTGAGCATCCA 321
DB 1875 GAGGACGTGGACGAGCTGCGCGGGAGGTGCAGATCATGACCACTCTCGGCGCAGGCC 1934
QY 322 AATGTTCTAGGATCAAGGACTTATGAAGATTCGATTCGTTGTTTCATATGTTATGGAG 381
DB 1935 AACGTGTGGCCCTCCGCGGCGGTACGAGGACCAAGCAGCGTGCACCTCGTCATGGAG 1994
QY 382 GTTGTGAAGGTGTGAGCTTTTGTGCGGATTTGTTCTAAGGTCTATTTTGTGAGCGT 441
DB 1995 CTGTGCGCGGCGGGAGCTCTTCGACCGCATCATCGCGGGCCAGTACACGAGCGC 2054
QY 442 GAAGCTGCAAGCTTATTAAGACATCTTGGTGTGTTGAGGCTTGTCTATCTCTTGGT 501
DB 2055 GCGCGCGGAGCTGCTGCGCGCCATCGTGCAGATCGTGCACACTCGCCACTCCATGGG 2114
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QY 562 AAGCTTAAGCTACCGATTTTGGTTGTCTGCTTCTTATTAAGCAGGACAAATTTATAT 621
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QY 622 GACCTAGTGAAGTCCGCTACTATGTTCCACAGAGGTCTTAAGAAATGTTATGAGCT 681
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DB 2295 GAGGCCGACATCTGGAGCGTGGCGTATGCTATCTATCTTCTTCCGCGGCGTCCCTCC 2354
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RESULT 13
US-09-347-801-3
; Sequence 3, Application us/09347801

Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 3
LENGTH: 2374
TYPE: DNA
ORGANISM: Oryza sativa
US-09-347-801-3

Query Match 10.9%; Score 189.6; DB 4; Length 2374;
Best Local Similarity 53.8%; Pred. No. 1.2e-38;
Matches 440; Conservative 0; Mismatches 369; Indels 9; Gaps 2;
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/ LENGTH: 1400 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: C-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Eimeria maxima
/ STRAIN: Houghton
/ DEVELOPMENTAL STAGE: sporozoite
/ IMMEDIATE SOURCE:
/ LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
/ CLONE: Em70-1
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1368
US-08-338-057-1

Query Match          9.4%; Score 165; DB 1; Length 1400;
Best Local Similarity 54.5%; Pred. No. 1.6e-32;
Matches 330; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

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Db 511 TAGGATGAGAAATGCGACGCTGCTGCTACGGGTGTTATCTCTATATCTCTCTCTGTT 570

QY 733 GTTCCCTCCCTTCTGGGAGAGAGTGTGGAATCTTTAGACAGATATTGCAAGGGAAG 792
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QY 793 TTAGATTTCAAATCTGACCGTGGCTACTATCTCAGAGAGCTCTAAAGATTGTATCTAT 852
Db 631 TTCACCTTCGATTTACACAGTGGCGTAGGTTAGCGAGCCAGCAAAAGATTTAATTAGG 690

QY 853 AAAATGCTGAAAGAGGCCCCAGAAACGATTTCTGCTCATGAAGCCTTGTCTCACCCA 912
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QY 913 TGGAT 917
Db 751 TGGAT 755
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Job time : 147 secs

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 08:01:19 ; Search time 475 Seconds

(without alignments)
3129.789 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	712.6	40.8	1635	9	US-09-938-842A-2344
4	643.4	36.8	1833	9	US-09-938-842A-2334
5	531.8	30.4	2230	10	US-09-828-313-26
6	507.8	29.1	1638	9	US-09-938-842A-1859
7	448.2	25.7	455	10	US-09-770-444-571
8	444.6	25.4	1602	9	US-09-938-842A-2304
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13	218	12.5	4162	9	US-09-988-462-26
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19	155	8.9	267	10	US-09-923-876-331

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Sequence 2657, Ap
Sequence 6, Appli
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Sequence 10, Appli
Sequence 7, Appli
Sequence 5432, Ap

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23 142.4 8.2 275 10 US-09-878-574-13205
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26 133.6 7.6 5637 10 US-09-001-835-82
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28 121.4 6.9 1383 9 US-09-935-464-2
29 121.4 6.9 1738 9 US-09-935-464-4
30 117 6.7 2061 12 US-10-096-960-1
31 117 6.7 3705 12 US-10-044-090-227
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33 112 6.4 257 10 US-09-878-574-7818
34 111.8 6.4 1551 9 US-09-925-299-210
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36 106.2 6.1 260 10 US-09-878-574-9200
37 105.6 6.0 270 10 US-09-294-093B-4541
38 105.6 6.0 1539 9 US-09-938-842A-162
39 104.8 6.0 855 9 US-09-938-842A-2190
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45 91.6 5.2 174 10 US-09-294-093B-5432

ALIGNMENTS

RESULT 1

US-09-938-842A-704
; Sequence 704, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ

; FILE REFERENCE: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 704

; LENGTH: 1488

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-704

Query Match

Best Local Similarity 85.0%; Score 1484.8; DB 9; Length 1488;

Mismatches 0; Predicted No. 0;

Matches 1488; Conservative 2; Indels 0; Gaps 0;

QY 67 ATGGAGACGAGCCAAACCCCTAGACGTCCTTCAAAACACAGCTTCTACCATATCAACACCA 126

Db 1 ATGGAGACGAGCCAAACCCCTAGACGTCCTTCAAAACACAGCTTCTACCATATCAACACCA 60

QY 127 CGATTAGACATCATACCTTCTGGGAAAAAGCTAGCCAAAGCCCAATTTGGAACAACC 186

Db 61 CGATTAGACATCATACCTTCTGGGAAAAAGCTAGCCAAAGCCCAATTTGGAACAACC 120

QY 187 TATCTCTGCACAGAGAAATCAACCTCGGCTAATACGCTTGAATCGAATCGATCCCGAGAGCG 246

Db 121 TATCTCTGCACAGAGAAATCAACCTCGGCTAATACGCTTGAATCGAATCGATCCCGAGAGCG 180

QY 247 AAGTCGTGTGCGGAGGATACGAAGATGATGGCGTGAGATTCAGATCATGATCAT 306
DB 181 AAGTCGTGTGCGGAGGATACGAAGATGATGGCGTGAGATTCAGATCATGATCAT 240
QY 307 CTTCTGAGCATCCAAATGTTCTTAGGATCAAAAGGAGCTTATGAAGATTCGGTGTGTT 366
DB 241 CTTCTGAGCATCCAAATGTTCTTAGGATCAAAAGGAGCTTATGAAGATTCGGTGTGTT 300
QY 367 CATATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTGATGCGATGTTCTTAAAGT 426
DB 301 CATATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTGATGCGATGTTCTTAAAGT 360
QY 427 CATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTTCTTGGTGTGTTGAGGCT 486
DB 361 CATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTTCTTGGTGTGTTGAGGCT 420
QY 487 TGTCTATCTCTTGGTGTATGATAGATGATCTCAACCTTGAGAAATTTCTTGTGTATAGT 546
DB 421 TGTCTATCTCTTGGTGTATGATAGATGATCTCAACCTTGAGAAATTTCTTGTGTATAGT 480
QY 547 CCTAAGATGATGCTTAAGCTTAAGCTACCGATTTTGGTGTGTTGCTCTCTCTATAGCCA 606
DB 481 CCTAAGATGATGCTTAAGCTTAAGCTACCGATTTTGGTGTGTTGCTCTCTCTATAGCCA 540
QY 607 GGACAATATTTATGACGTAGTGAAGTCCGTACTATGTTGCACAGAGGTGCTTAAAG 666
DB 541 GGACAATATTTATGACGTAGTGAAGTCCGTACTATGTTGCACAGAGGTGCTTAAAG 600
QY 667 AAATGTTATGGACCTGAATAGATGTTGGAGTGTGTTGTTTATCTCTACATTTTACTC 726
DB 601 AAATGTTATGGACCTGAATAGATGTTGGAGTGTGTTGTTTATCTCTACATTTTACTC 660
QY 727 AGCGTGTCTCTCCCTTCTGGGAGAGATGAGTCTGGAACTTTTACAGATATTGCAA 786
DB 661 AGCGTGTCTCTCCCTTCTGGGAGAGATGAGTCTGGAACTTTTACAGAGATATTGCAA 720
QY 787 GGAAGTTAGATTCAAACTGACCGGTGGCCCTACTATCTCAGAACTGCTAAAGATTG 846
DB 721 GGAAGTTAGATTCAAACTGACCGGTGGCCCTACTATCTCAGAACTGCTAAAGATTG 780
QY 847 ATCTATTAATGCTCGAAGAGGCCCCAAGAACGGATTTCTGCTATGAGCCTTGTGT 906
DB 781 ATCTATTAATGCTCGAAGAGGCCCCAAGAACGGATTTCTGCTATGAGCCTTGTGT 840
QY 907 CACCATGAGATTGTCGATGAACAGCAGCACCAGACAGCCTCTTGATCAGCAGTCTTA 966
DB 841 CACCATGAGATTGTCGATGAACAGCAGCACCAGACAGCCTCTTGATCAGCAGTCTTA 900
QY 967 TCTCGTCTAAGCAGTTTCTCAAAATGAATTAAGATTAAAGAAATGGCATTTACGGGTAA 1026
DB 901 TCTCGTCTAAGCAGTTTCTCAAAATGAATTAAGATTAAAGAAATGGCATTTACGGGTAA 960
QY 1027 GTCAGAGACTTTCAGAGGAGAAATTTGGAGTCTGAAGGAATTTGTTCAAGATGATAGAC 1086
DB 961 GTCAGAGACTTTCAGAGGAGAAATTTGGAGTCTGAAGGAATTTGTTCAAGATGATAGAC 1020
QY 1087 ACAGACAACAGCGGAGGATTTCTTGAAGAGTCAAAAGCGGTTTGAAGAGAGTCCGA 1146
DB 1021 ACAGACAACAGCGGAGGATTTCTTGAAGAGTCAAAAGCGGTTTGAAGAGAGTCCGA 1080
QY 1147 TCTGAAGTATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAACAGT 1206
DB 1081 TCTGAAGTATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAACAGT 1140
QY 1207 GGTACAATAGACTACGGGAGAAATTTCTAGCAGCAACCTTTACACATGAACAAGATGAGAGA 1266
DB 1141 GGTACAATAGACTACGGGAGAAATTTCTAGCAGCAACCTTTACACATGAACAAGATGAGAGA 1200
QY 1267 GAGGAGATTTCTGGTGTGATTTTTCGACATTTTTCGACATTTGACAAGACGGAAGCGGTTATATCACC 1326
DB 1201 GAGGAGATTTCTGGTGTGATTTTTCGACATTTTTCGACATTTTTCGACATTTTATATCACC 1260

QY 1327 ATCGATGAGCTTCAGTCAAGTTGCACAGATTTGCTCTATGTGATACACCTCTGACGAC 1386
DB 1261 ATCGATGAGCTTCAGTCAAGTTGCACAGATTTGCTCTATGTGATACACCTCTGACGAC 1320
QY 1387 ATGATCAAGGAGATTCATCTTGACAAATGACGGGAAGATCGATTCTCGAGGTTTACAGCA 1446
DB 1321 ATGATCAAGGAGATTCATCTTGACAAATGACGGGAAGATCGATTCTCGAGGTTTACAGCA 1380
QY 1447 ATGATGAGAAAGAGATGGAGTTGGGAGAGACAGAACCATGATGAAGAACTTGAACTTC 1506
DB 1381 ATGATGAGAAAGAGATGGAGTTGGGAGAGACAGAACCATGATGAAGAACTTGAACTTC 1440
QY 1507 AACATGCTGATGCTTTTGGAGTTGATGCTGAAGAACTCTGATGACTGA 1554
DB 1441 AACATGCTGATGCTTTTGGAGTTGATGCTGAAGAACTCTGATGACTGA 1488

RESULT 2
US-09-938-842A-786
; Sequence 786, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 786
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-786

Query Match 42.6%; Score 744.2; DB 9; Length 1473;
Best Local Similarity 70.0%; Pred. No. 8,6e-173;
Matches 1001; Conservative 0; Mismatches 428; Indels 0; Gaps 0;

QY 106 GTTCTACCATATCAACACACCACGATTAAAGAGATCAATACCTTCTGGGAAAAAGCTAGGC 165
DB 28 GTTCTTCTTACAGACCAAAAGGTTGAAGACAATTTACTTTCTTGGTCAAGTCTTGA 87
QY 166 CAAGGCCAAATTTGGAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTAGGCC 225
DB 88 CAAGGCCAAATTTGGAACAACCTATCTCTGTACCCATTAACACAGACAGCTAAAAGCTGGC 147
QY 226 TGCAAATCGATCCGAGCGAAAGCTCGTGTGCGGAGGATTACGAGATGTATGGCGT 285
DB 148 TGCAAATCGATCCGAGCGAAAGCTCGTGTGCGGAGGATTACGAGATGTATGGCGT 207
QY 286 GAGATTCAGATCATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGAGGACT 345
DB 208 GAGATTCAGATCATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGAGGACT 267
QY 346 TATGAAGATTCGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 405
DB 268 TACGAGGACACAAAACGTCATCTTGTGATGGAGCTTTGTGAAGGAGGTGAGTGTGTT 327
QY 406 GATCGGATTTCTTAAGGCTCATTTAGTGAGCGTGAAGCTGCAAGCTTATTAAAGACG 465
DB 328 GATGAAGATTTGAAGAGAGGTCATTTACAGTGAAGAGAGAGCTGCTAGCTTATCAAGACC 387
QY 466 ATTCTTGGTGTGTTGAGGCTTGCTATTCTCTTGGTGTGTTGATGATGATGATGATGATGAT 525

Db 388 ATGTGGGGTGTGAGCGGTGTCACCTCTGTGGTGTGTCATAGAGATCTTAAGCCT 447
QY 526 GAGAAATTTCTTGTGTAGTCTTAAGAAGATGATGTAAGCTTAAGGCTACCGATTTTGT 585
Db 448 GAGAAATTTCTTGTGTAGTCTTAAGAAGATGATGTAAGCTTAAGGCTACCGATTTG 507
QY 586 TTGTCTGTCTTATAAGCCAGGACAATATTAATGAGCTAGTGTGGAAGTCCGTACTAT 645
Db 508 CTCTCTGTCTTCTGACACCGAGGAGCAATTTTCGAACTCGTGTGGTAGTCTTACTAT 567
QY 646 GTTGACACAGAGTCTTAAGAAATTTATGACCTGAATAGATGTGTGGAGTCTCTGT 705
Db 568 GTGGCACTGAGTTTACATAAGCATATGCTCTGATGTGAGCTATGAGTCTCTGA 627
QY 706 GTTATCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCTGGGACAGACTGAGTCTGA 765
Db 628 GTTATCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCTGGGACAGACTGAGTCTGA 687
QY 766 ATCTTTAGACAGATTTCAAGGGAAGTTAGATTTCAATCTGACCTGGCTTACTATTC 825
Db 688 ATCTTCAGAGATTTTACAGGGAAGTTGAGTTTGAATCAATCTTGGCTTACTATTC 747
QY 826 TCAGAAGCTGCTAAGATTTTATCTATAAATGCTCGAAAGGAGCCCAAGAAACGCAT 885
Db 748 TCAGAGAGTGCCTAAGATTTTATTAAGAAATGCTTGAAGCAATCTTAAGAGGCTA 807
QY 886 TCTGCTCATGAAGCTTGTGTCACCATGATGATGTCGATGAACAGACGACCAAG 945
Db 808 ACTGCTCATGAAGTGTGTCATGCTGCTGATGTTGGATGATGAAGTTGCTCCAGATAA 867
QY 946 CCTCTTGATCCAGAGCTTATCTGCTTAAGCAGTTTCTCAAAATGAATTAAG 1005
Db 868 CCTTTGACTCGCGGTAGTGTCCGCTGGAAGTTTCTGCAATGAACAACTTAAG 927
QY 1006 AAATGGCATTCGCGTAATTTGCTGAGAGCTTTTCAAGGAAGAAATGGAGTCTGAAG 1065
Db 928 AAGATGGCTTTACGAGTATTTGACAGAGACTATCTGAGGAAGAAATCGGTGCTCAA 987
QY 1066 GAATTTGTCAGATGATAGACAGACAGACAGCGGACGATTAATTTTGAAGAGCTCAA 1125
Db 988 GAATTTGTCAGATGATAGACAGACAGATTAAGTGGGACTATCAGCTTTGAAGAGTTAAA 1047
QY 1126 GCGGGTTTGAAGAGAGTGGATCTGAATGATGAATCAGAAATCAAGTCTCTCATGAT 1185
Db 1048 GATAGTATGAGACGCTTTGGTCTGAGCTTTATGGAATCAGAGATCCAGACTCTTGGGT 1107
QY 1186 GCGCTGATATCGACAGTGGTACAAATGATGATGATGATGATGATGATGATGATGAT 1245
Db 1108 GCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1167
QY 1246 CACATGAACAGATGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1305
Db 1168 CACTTGACAGCTGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1227
QY 1306 GAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365
Db 1228 GATGCAAGTGTATACATCACTATCGAAGAGCTTCAACAGGATGGAAGAGTGGTATA 1287
QY 1366 TGTGATACACTCTGGAGCAGATGATCAAGAGATGATGATGATGATGATGATGATGAT 1425
Db 1288 AAGCATCTAATCTGATGAATGATCAAGAGATGATGATGATGATGATGATGATGATGAT 1347
QY 1426 GATTTCTCGAGTTTACAGCAATGATGAGGAAGGATGATGATGATGATGATGATGATGAT 1485
Db 1348 GACTATGGAATTTTGGCAATGATGAGGAAGGATGATGATGATGATGATGATGATGAT 1407
QY 1486 ATGATGAAGACTTGAACCTTCAACATGCTGATGCTTTTGGAGTTGAT 1534
Db 1408 CGGAGAACTATGAGAACTCTCTCACTTTGGAACTACTCTTCTCTGAT 1456

RESULT 3

US-09-938-842A-2344
; Sequence 2344, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2344
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2344

Query Match 40.8%; Score 712.6; DB 9; Length 1635;
Best Local Similarity 68.3%; Pred. No. 5.3e-165;
Matches 988; Conservative 0; Mismatches 459; Indels 0; Gaps 0;
QY 73 ACAGAGCCAAACCCCTAGACGCTTCAACACAGTTCACCATATCAACACCCAGATTA 132
Db 184 ATGGCGGTAACTGTGACATCAATCTTACTATGTCTTGTGTCACAGACTCTTAACAT 243
QY 133 AGAGATCATTAACCTTCTGGGAAAAGCTAGCCCAAGCCAAATTTGGACACCACTATCTC 192
Db 244 CTTGATCTTTACAGCTTGAGTCGTAAGTTAGGACAAAGCAATTCGGGACCACTATTTG 303
QY 193 TGCACAGAGAAATCAACCTCCGCTAAATATACGCTGCAAAATCGATCCCGAGCAAGGCTC 252
Db 304 TGTACTGATATTCACAGAGGTGTGACTATGCTTGTAGTCTATATCAAGAGAAATG 363
QY 253 GTGTGTCGCGAGGATTCAGAGATGATGCGGTGAGATTCAGATTCAGATTCATCTCTCT 312
Db 364 ATATCTAAAGAAAGTGTAGGATGTTAGGAGGAGATTCAGATTAATGATCTTACTAGCT 423
QY 313 GAGCATCCAAATGTGTAGGATCAAGAGGACTTATGAAGATTCGCTGTTGTTTCATATT 372
Db 424 GGTCAAGAAATATTTACTATTAAGAGGCTTATGAGGATCCTTTGTAIGTTACATT 483
QY 373 GTATGAGGTTTGTGAAGTGTGAGCTTTTTCGATCGGATTTTCTTAAGGTCATTTT 432
Db 484 GTGATGAGCTTTGTGCTGGTGGTGGTGTGTTGATAGGATTTATCATAGAGTCAATAC 543
QY 433 AGTCAGCGTGAAGCTGTCAGACTTATTAAGACGATTCCTTGGTGTGTTGTTAGGCTTGCAT 492
Db 544 AGCCAGGAAAGCTGCTGAGTTGACCAAGATCAATTCGCTGTTGTTGTTAGGCTGTCAT 603
QY 493 TCTCTTGGTGTATGATAGAGATCTCAACCTGAGAAATTTCTTGTGTTGATAGTCCCTAAA 552
Db 604 TCCTTGGTGTATGATAGAGATTTAAAGCTTGAAGATTTCTTGTGTTGTTAATAGGAT 663
QY 553 GATGATGCTTAAGCTTAAGCTTACCGATTTTGGTTTGTCTGCTCTTATAGCCAGGACAA 612
Db 664 GATGATTTCTCTCTTAAGGCAATTTGATTTTGGTCTCTCTCTTCTTCARACACCGCCAA 723
QY 613 TATTATATCACCTAGTGTGAAGTCCGATCTACTATGTTGACCCAGGAGTGTCTAAAGATGT 672
Db 724 ATATCAAGATGTTTGGAAAGTCCATATGTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 783
QY 673 TATGGACCTGAATAGATGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Db 784 TATGGTCCAGAACTGATGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843

QY	733	GTTCTTCCCTTCGTGGCGCAGAGACTGAGTCTGGAATCTTTTAGACAGATATTTCGAAGGGAAG	792
Db	844	GTCCCGCCCTTCTGGCGAACAACACAGCAAGAATAATTTGATGCTGTGTTGAAGGGATAT	903
QY	793	TTAGATTTCAAATCTCACCCGTGGCGCTACTATCTCAGAAAGTGCTAAAGATTTTGCATCTAT	852
Db	904	ATTGACTTTGATACAGACCCTGGCCCTGTCATATCCGACAGTCTTAAGATCTGATCCGG	963
QY	853	AANAATGCTCGAAGAGGCCCAAGAAAACGCAATTTCTGCTCATGAAGCGCTTGTCACCCA	912
Db	964	AAGATTTATGCTCTAGTCTCTCTGAAGGTTTGACTGCTCATGAAGTCTTTCGCGTCATCCA	1023
QY	913	TGGATTGTCGATGAACAAGCAGCACACAGANGCCTCTTGATCCAGCAGTCTTATCTCGT	972
Db	1024	TGATCTGTGAGATGGAGTTGCCCGGATAGAGCACATGACCCGGCTGTTTTGCTCTCGT	1083
QY	973	CTAAGCAGTTTTTCTCAAATGAATAAGATTAAAGAAAAATGSCATTACGGGTAAATPGCTGAG	1032
Db	1084	CTAATAACAGTTTTCTCAATGAATAAATTAAGAAGATGGCTTTAAAGGTGATAGCTGAG	1143
QY	1033	AGACTTTCAGAGGAAGAAATTCGAGGTCTGAAGGAATTTGTTCAAGATGTATGACACACAGAC	1092
Db	1144	AGCCTCTCAGAAGAAGAGATTCGGGTTTAAAGCAATGTTTGAGGCAATGGATFACTGAT	1203
QY	1093	AACAGCGGAACGATTACTTTTGAAGAGTCTAAAGCGGTTTGAAGAGAGTCGGATCTGAA	1152
Db	1204	AACAGCGGTCAATCACTTTTGATGAACCTCAAAGCTGGCTTTGAAGAAGATATGGATCAACC	1263
QY	1153	CTGATGGATCAGAAATCAAGTCTCTCATGNTGCGGCTGATATCGCACACAGTGGTACA	1212
Db	1264	TTGAAGAACCAGAGATCCGAGATCTTATGGAAGCGGCTGATGTGGACAACACGCGGTACA	1323
QY	1213	ATAGACTACGGAGAAATTCCTAGCAGCAACTTACACATGAACAAGTGGAGAGAGAGGAG	1272
Db	1324	ATAGATTACAGCGAGTTTATTCAGCGGAGTCCATCTGATTAACATAGAGAGAGAGAG	1383
QY	1273	ATTCTGGTGGCTGCATTTTCGGACTTTGACAAGACGGAAGCGGTATATACCATCGAT	1332
Db	1384	CATCTTGTCTCTGCATTTTCAGTACTTTGACAAGAATGAAGTGGTTTACATCACCATTGAT	1443
QY	1333	GAGCTTCAGTCAGCTTGACAGAGTTTGGTCTATGTGATACACCTCTGGAGCAGCATGTC	1392
Db	1444	GAGCTGCACAACTCTTGCAATTTGAACATGGATGACCGGATGTTTTTCTTGAGACATTAATC	1503
QY	1393	AAGGAGATTGATCTTGACAATGACGGGAAGATPCGATTTTCTCGGAGTTTTCAGCAATGATG	1452
Db	1504	AAAGAAGTAGATCAAGACAAACGATGGCGGATTGATTACGAAGAATTTGTTGGCATGATG	1563
QY	1453	AGAAAAGGAGATGGAGTTGSGGAAGACGACACCATGATGAAGAACTTGAACCTTCAACATT	1512
Db	1564	CANAGGGAATGCTGGTGTAGGGAGAAGAACATGAAAAATAGTCTAAACATCAGCATG	1623
QY	1513	GCTGATG 1519	
Db	1624	AGAGATG 1630	

RESULT 4

US-09-938-842A-2334
; Sequence 2334, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPL300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866

Db 1185 AAGGTTAACTGCCACCAAGTAATATGTCATCCATGGTTCAAGTCGACGGTGTGGCTCC 1244
QY 939 AGAAGAGCCCTTGTATCCAGCAGCTTATATCCTGCTTAAGCAGTTTCTCAAAATGAATA 998
Db 1245 AGAAGAGCCCTTGTATCCAGCAGCTTATATCCTGCTTAAGCAGTTTCTCAAAATGAATA 1304
QY 999 GATTAAAGAAATGGCAATACCGGTAATGCTGAGAGACTTTCAGAGAAAGAAATGGAGG 1058
Db 1305 GTTCAAGAAATGGCTTTAGAGTCAATGCTGAGAGCTTATCTGAAGAAAGAAATGGCGGG 1364
QY 1059 TCTGAAGAAATGTTCAAGATGATAGACACAGACAGCGGGAAGGATTTACTTTTGAAGA 1118
Db 1365 CTGGAAGAAATGTTTAAATATGATAGATGCGGCAAGAGTGGTCAGATAACTTTTGAAGA 1424
QY 1119 GCTCAAGAGCGGTTTGAAGAGTGGATCTGAACTGATGGAATCAAGAAATCAAGTCTCT 1178
Db 1425 ACTGAAGAGCAGGACTAAACAGGTAGGGGCAATCTCAAGAGGCTGAAATTTCTCGACT 1484
QY 1179 CATGGATGCGGCTGATATCGACACAGTGGTACAAATAGACTACGGGAATTCCTAGCAGC 1238
Db 1485 GATGCAAGCTGCTGATGCGGACACACCGGACAAATAGATTAACAGAGTTTATAGCTGC 1544
QY 1239 AACCTTACATGAACAAGATGAGAGAGAGGAGATTTCTGGGCTGCATTTTTCGGACTT 1298
Db 1545 AACATTACATCTAAACAAATAGAGAGAGAGGACCAATTTGTTTCAGCCCTTACATACTT 1604
QY 1299 TGCAAAAGCGGAGCGGTTATATCCATCATCGATGAGCTTCAGTCACTTGCACAGATT 1358
Db 1605 TGCAAAAGTGGAGCGGCTTATATCAACCCAGAGAGGCTTCAACAGGCTTGTGAGGATT 1664
QY 1359 TGTCTATGATACACCTCTGGACGACATGATCAAGGAGATTGATCTTGACAAATGACGG 1418
Db 1665 TGTGTTGAGGATGTCGCGATAGAGAACTGATCGCGGATGTTGATCAAGAAATGACGG 1724
QY 1419 GAAGATCGATTTCTCGGAGTTTACAGCAATGATGAGGAAGAGAGATGGAGTTGGGAGAAG 1478
Db 1725 GCGAATAGACTCAACAGGTTTGTGGGATGATGCGAAGAGAGCAATCACAGGAGACC 1784
QY 1479 CAGAACCATTGATGAAGAACTTGAACCTTCAACATTGCT 1515
Db 1785 TGTGAATGGGCTAGAGAAAGCTTTAGCAATGCT 1821

RESULT 5

US-09-828-313-26
; Sequence 26, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2230
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-313-26

Query Match 30.4%; Score 531.8; DB 10; Length 2230;
Best Local Similarity 62.5%; Pred. No. 1.7e-120;
Matches 849; Conservative 0; Mismatches 507; Indels 3; Gaps 1;

QY 141 TTACTCTTCTGGGAAAAAGCTAGCCCAAGGCCAAATTTTGGAAACACCTATCTCTGCACAGA 200
Db 602 TTACATCTCTGGGAGCGGAGCTTGGCCGAGGCGAGTTCGGAGTACTTACTTGTGTACTGA 661
QY 201 GAATCAACCTCCCTATATACGCTGCAAAATCGATCCGAGAGGAAAGCTGCTGTGTGCG 260
Db 562 CAAGATGACGATGAGCGGTACGCGTCAAGAGATCGCCAAAGCGAACTGACAGTAA 721
QY 261 CGAGGATTAAGAGATGATGGCGTGAGATTCAGATCATCATCTCTCTGAGCATCC 320
Db 722 GGAGGATTAAGAGATGATGGCGTGAGATTCAGATCATCATCTCTCTGAGCATCC 781
QY 321 AAATGTTTGTAGGATTAAGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 380
Db 782 CAATATCGTGTGTAAAGGATGTTTCGAGGACAGCATTCCTGCACTTCTGTGATGA 841
QY 381 GGTGTTGAAAGTGGTGTGATCGGATTTTGTGATCGGATTTTCTAAAGGTCATTTTGTAGTGAGCG 440
Db 842 GCTCTGTGAGGTTGGCGAGCTCTTCGATCGCATCATTCGCCAAGGGGATTTACAGTGAGCG 901
QY 441 TGAAGCTGTCAAGCTTATTAAGAGATTCCTTGTGTTGTTGAGGCTTGTCTCTCTCTG 500
Db 902 CGCGCTGCGGATATGTCAGAGTCACTCAATGTCGACAGATGCCACATCATTTAGG 961
QY 501 TGTATGATAGAGATCTCAAACTGAGAAATTTCTTCTTGTGATAGTCTCTAAAGATGATGC 560
Db 962 GGTCTTCATCGGATCTCAAGCCAGAGAAATTTCTTGTGCGCCAGGAGCTGAGGATGC 1021
QY 561 TAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 620
Db 1022 GCTCTGAAAGCCACAGACTTCGCTGCTCAACTTTTAAAGCCAGGATGTTGTCTCA 1081
QY 621 TGAGCTAGTTGGAAGTCCGCTACTATGTCAGAGAGTCTTAAAGAAATGTTTATGAGCC 680
Db 1082 GGATATGTTGGAAGTCCGCTACTATGTCAGAGTCTTAAAGAAATGTTTATGAGCC 1141
QY 681 TGAATAGATGTTGAGAGTCTGCTGTTTATCTCTTACATTTTACTCAGCGGTTTCTCTCC 740
Db 1142 TGAAGCTGATGTTGAGAGTCTGAGGCTGATGTTGTTGATCTCTGCTGCTGTACCC 1201
QY 741 CTCTGCGCAGAGCTGAGTCTGGAATCTTTAGACAGATATTCAGAGGAGTATGATTT 800
Db 1202 CTCTGCGCTGAACTGAGCAGGATCTTTGAGCTGTCTCAAGGGGACATAGACTT 1261
QY 801 CAAATCTGACCCCTGGCTACTATCTCAGAGAGTCTTAAAGATTTGATCTTATAAATGCT 860
Db 1262 CGAGAAAGATCTCCATGCGGAAATCTCCAACGGGCTTAAAGATTTGTTGAGGAAATGCT 1321
QY 861 CGAAGGAGCCCCAAGAAAGCAATTTCTGCTCATGAAGCCTTGTGTCAACCCATGATGTT 920
Db 1322 AAACCTTAAAGTGAAGATAGCTCTGAGCGCACAGAGTGTGTAAGCATCCATGATGAA 1381
QY 921 CGATGAACAGCAGCAGCAGCAAGCTCTTGTATCAGCAGTCTTATCTGCTCTAAGCA 980
Db 1382 GGAAGATGTTGATGCTCCAGAGCTGCTGACATCGGCTGTTGACAGAGCTGAGAAA 1441
QY 981 GTTTCTCAAAATGAATAGATTAAGAAATGCAATTTACGGTAAATGCTGAGAGACTTTC 1040
Db 1442 TTTCTCAGCGCGCAACAAGATGAAAGAGTGGCGCTGAAAGTGTGAGAGAGTCTGTC 1501
QY 1041 AGAGGAAAGAAATGAGGCTCTGAAGAAATGTTCAAGATGATAGACACAGACAGACGG 1100
Db 1502 GGAGGAAGAGATCGTGGGTTGAGGAGATGTTCAAAATCCATAGATACAGACAGCGG 1561
QY 1101 AACGATTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTGGATGCACTGATGCA 1160
Db 1562 CACGGTGAAGCTTGAAGAGGTTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAG 1621
QY 1161 ATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAAACAGTGTGATACACTA 1220
Db 1622 ATCGGACATCAGAAACTAATGGAAGCTCAGATGCGATGGAAGCGGCAAGATCGACTT 1681
QY 1221 CGGAGATTTCTAGCAGCAACCTTACATGATGAACAGATGAGAGAGAGGATTTCTGTT 1280

Db 1682 CAACGAGTTCATATCGGCAACAATCCATGAACAAGCGGAGAAGAGGATCACCTTTG 1741
QY 1281 GCGTCATTTTCGGACTTTGACAAAGACGGAAGCGGTTATATCAACATCGATGAGCTTCA 1340
Db 1742 GGCACATTCATGCATTTTCGACACGGAACAATAGCGGGTATATCACCATCGGAGACTTCA 1801
QY 1341 CTCACATTCGACAGAGTTTGGTCTTATGTATAC---ACCTCTGGACGACATGATCAAGAA 1397
Db 1802 GGAAGCAATCGGAAGAATGGAATGGAGATCCTGAGACACATCCCAAGAGATCATCAGGGA 1861
QY 1398 GATTGATCTTGACATGACGGAAGATCGATTCTCGGAGTTTACAGCAATGATGAGAA 1457
Db 1862 GTGGACACACACACGCGGAGGAATAGACTACGACGAGTTCGTAGCCATGATCGGCA 1921
QY 1458 AGGAGATGAGTGGGAGAGACAGACCATGATGAAGAA 1496
Db 1922 GGGCAATCTCGCGCTGAAACCGGAGGAAACGGTGAACAA 1960

RESULT 6

US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Query Match 29.1%; Score 507.8; DB 9; Length 1638;
Best local similarity 61.7%; Pred. No. 1.1e-114;
Matches 828; Conservative 0; Mismatches 507; Indels 6; Gaps 1;
QY 131 TAAGAGATCATTAACCTCTCTGGAAAAAGAGTAGGCCAAGGCCAAATTTGGAACAACCTATC 190
Db 176 TCAGCGCAAAATACATCTTAGTCTGCTGAATTAGTTCGAGCGGAATTCGGAATCACATTAC 235
QY 191 TCTGCACAGAGAATCAACCTCCGCTAAATACGCTCAAAATCGATCCCAAGCGGAAAGC 250
Db 236 TCTGTACTGATCGTGAACCCACGAGCTTTAGCTTCAAAATCGATTTCAAGCGGAAAGC 295
QY 251 TCGTGTCTCGGAGGATGACAGAGATGATGGGTGAGATTCAGATCATCATCTCT 310
Db 296 TTCGAACAGCTGTGATATCGAAGACCTTCGTCTGAGGTAGCGATTATCTACTATTAC 355
QY 311 CTGAGCATCCAAATGTTGTAGGATCAAGAGGACTTATGAGATTCGGTGTTCCTTCATA 370
Db 356 CTGAGCATCCAAAGATGATTAAGCTTAAGCTAGTTATGAGGATTAACGAACGTGATC 415
QY 371 TTGTTATGGAGGTTGTGAAGTGGTGGTCAAGCTTTTGTATCGGATTTCTTAAAGGTCATT 430
Db 416 TGGTTATGGAGCTTTGTGAAGGAGGTGAGCTTTTGTATCGGATTTGTCTAGAGACATT 475
QY 431 TTAGTACGCGGAGAGCTGTCAGGCTTTATTAAGACGATCTTGGTGTGTGAGGCTTGTC 490

Db 476 ACACGAGCGTGCTGCTGAGCTGTTGCGAGAACGATTTGCTCAGGTTGTGATGATGTGC 535
QY 491 ATTCTCTTGGTGTATGATGATGATCTCAAACTCGAGAAATTTCTGTTTGTATGATCTCTA 550
Db 536 ACTCTAATGGAGTTATGATGATGATTTGAAACCTCGAGAAATTTCTGTTTGTATGATCTCTA 595
QY 551 AGATGATGCTTAAGCTTAAGGCTACCGATTTGGTGTCTGCTCTCTATAGCCAGGAC 610
Db 596 AGGAAATTCACCAATGAGGCTATTGATTTGGCTTGTCTGCTCTCTCAAACTCGGAG 655
QY 611 AATATTTATATGACCTAGTTGGAAGTCCGCTACTATGTCACACAGAGTGTCTAAAGAAAT 670
Db 656 ATAACTTTACAGAGATTTAGGAAGTCCGCTATTAATATGCTCCCAAGATTTTGAAGAG 715
QY 671 GTTATGGACCTGAATATGATGTTGAGTGTGCTGCTGCTCTCTCTACATTTTACTTCAGG 730
Db 716 ATTATGGACCGAGGTTGATGTTGAGTGTGCGGAGTTATTAATCTATATCTTCTGCTGTG 775
QY 731 GTGTTCTCTCCCTTCTGGGACAGAGCTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGA 790
Db 776 GTGTTCTCTCCCTTCTGGGCTGAGACTGAACAGGTGTGCTCTTGGATCTTTCGGGAG 835
QY 791 AGTTAGATTTCAAACTGACCGTGGCTTACTATCTCAGAACTGCTTAAAGATTTGATCT 850
Db 836 TTCTTGATTTTAAGAGAGACCTTGGCTTCAGATATCAGAGAGTGCACAGAGCCCTTGTGA 895
QY 851 ATAAATGCTCGAAAGGAGGCCCAAGAAAGCATTTCTGCTCATGAAGCTTTGTGTCACC 910
Db 896 AGCAGATTTGGATCTGATCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
QY 911 CATGATTTGCTGATGAACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 970
Db 956 CATGATACAGAAATGCAAGAAAGCTCCCAATGTTCTCTTAGAGATATAGTCAGATCTA 1015
QY 971 GTCTAAAGCAGTTTCTCAAAATGAATAAGATTAAGAAATGCGATTTACGGGTAATGCTG 1030
Db 1016 GGTGAAGCAGTTCTCTATGATCAACAGATTTCAAAAGAAAGTTCTCTGTTAAATTCGG 1075
QY 1031 AGAGACTTTCAAGAGGAAAGATTTGAGGCTGCTGAAGAAATTTCAAGATGATAGACACAG 1090
Db 1076 AGCATTGTCTATTCAAGAGTTGAAGTATTAAGAACATGTTCTCACTGATGGATGATG 1135
QY 1091 ACAACAGCGGACGATTTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTGGGATCTG 1150
Db 1136 ACAAGGATGTTAAATAAATTAACCTTACCCGAACTCAAGCTGGCTTCAGAAAGTGGTTCAC 1195
QY 1151 AACTGATGGAATCAGAAATCAAGTCTCTCATGATGCTGCTGATATCGACACAGTGTGA 1210
Db 1196 AACTGTTGAACAGAGATCAAAATGTTGATGAAGTGGCGGATGCTGATGGAATGGGT 1255
QY 1211 CAATAGACTACGAGAGATTTCTAGCAGCAACCTTACACATGAACAGATGGAGAGAGG 1270
Db 1256 TTCTGGATTTAGAGAGTTTGTAGCTGTGATAATTCATTTGCAAGAGATAGAGATGATG 1315
QY 1271 AGATTCGTGGTGGCTGATTTTCGAGCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1330
Db 1316 AACTTTTCAACATAGCTTTTATGTTTTCGACAAAGATGAAGTACATACATTTGAAGT 1375
QY 1331 ATGAGCTTCACTGAGCTTTCACAGA-----GTTTGTCTATCTGTATACACCTTGGAG 1384
Db 1376 ATGAGTACGGGAGCTTTTACGGGATGAGTTAGCGAGCCAGAGCCAGTGTCTAAGCG 1435
QY 1385 ACATGATCAAGGAGATTTGATCTTGAATGACGGGAGATCGGATTTCTCGGAGTTTACAG 1444
Db 1436 ACATGATCGGTGAATTTGACACTGACAGGAGCGGACGTATATAACTATGATGAGTTTGTGA 1495
QY 1445 CAATGATGAAGAGGAGATG 1465
Db 1496 CGATGATGAAGCTGGAACGTG 1516

RESULT 7
US-09-770-444-571

; Sequence 571, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09770.444
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-571

Query Match 25.7%; Score 448.2; DB 10; Length 455;
Best Local Similarity 98.9%; Pred. No. 2.2e-100;
Matches 450; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 999 GATTAAAGAAATGCGATTACGGGTAAATGCTGAGAGACTTTTCAGGAGAAATTTGGAGG 1058
Db 1 GATTAAAGAAATGCGATTACGGGTAAATGCTGAGAGACTTTTCAGGAGAAATTTGGAGG 60
QY 1059 TCTGAAGGAATTTTCAAGATGATAGACACAGACAGCGAAGGAGATTACTTTTGRAGA 1118
Db 61 TCTGAAGGAATTTTCAAGATGATAGACACAGACAGCGAAGGAGATTACTTTTGAAGA 120
QY 1119 GCTCAAGCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCT 1178
Db 121 GCTCAAGCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCT 180
QY 1179 CATGGATGCGGCTGATATCGACACAGTGGTACAAATGATACGAGAAATTCCTAGCAGC 1238
Db 181 CATGGATGCGGCTGATATCGACACAGTGGTACAAATGATACGAGAAATTCCTAGCAGC 240
QY 1239 AACCTTACATGAACAAAGATGGAGAGAGGAGATTCTGGTGGCTGCATTTTCGGACTT 1298
Db 241 AACCTTACATGAACAAAGATGGAGAGAGGAGAAATCTGGTGGCTGCATTTTCGTAATT 300
QY 1299 TGACAAAGCGGAAGCGGTTATATCACCATGATGAGCTTCAGTCAGCTTCACAGAGATT 1358
Db 301 TGACAAAGCGGAAGCGGTTATATCACCATGATGAGCTTCAGTCAGCTTCACAGAGATT 360
QY 1359 TGGTCTATGTGATACACTCTGGACGACATGATCAAGAGATTTGATCTTGACAAATGACGG 1418
Db 361 TGGTCTATGTGATACACTCTGGACGACATGATCAANNAGATTGATCTTGACAAATGACGG 420

QY 1419 GAAGATCGATTCTCGGAGTTTACAGCAATGATGA 1453
|||||
Db 421 GAAGATCGATTCTCGGAGTTTACAGCAATGATGA 455
RESULT 8
US-09-938-842A-2304
; Sequence 2304, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938.842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2304
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2304

Query Match 25.4%; Score 444.6; DB 9; Length 1602;
Best Local Similarity 59.7%; Pred. No. 3.6e-99;
Matches 788; Conservative 0; Mismatches 524; Indels 9; Gaps 2;

QY 142 TACCTTCGCGGAAAGAGCTAGGCCAAGCCAAATTTGGAACAACCTATCTCTGACACAGAG 201
|||
Db 169 TATGATCTGGGCGGTGAGGTGGTGGCGGAGAGTTTGGTATTACTTACTTGTGCACTGAT 228
QY 202 AAATCAACTCCGCTAATTACGCTGCAATCGATCCGGAAGCAAGCTCGTGTGCGC 261
|||
Db 229 ATCAAAAGCGGCGAAGATGCGTGCAGTCTATATCAAGAAGAGCTTAGAACAGCT 288
QY 262 GAGGATTACGAAGATGTATGCGGTGAGATTCAGATCATCATCTCTGAGCATCCA 321
|||
Db 289 GTGATATAGAGGATGTAGGAGGGAAGTTGAGATAATGAACATATGCCATAGACACCA 348
QY 322 AATCTTGTAGGATCAAGGGAAGCTTATGAAGATTGCGGTGTTGTTTCATATTTGTTATGGAG 381
|||
Db 349 AATATCGTGTGCGTGAAGGATGCGCTTTGAGGATGATGATGCGATATAGTTATGGAG 408
QY 382 GTTGTGAAGGTGCTGAGCTTTTGTGCGGATTTGTTCTAAAGGTCAATTTTGTGAGCGT 441
|||
Db 409 TTGTGTGAAGGAGGTGAGCTTTTGTGCGGATTTGCTGAGAGCTCATTTACTGAGCGA 468
QY 442 GAAGCTGTCAAGCTTATTAAGACGATTCTTGGTGTGTTGTTGAGGCTTGTCTCTTTGGT 501
|||
Db 469 GCTGCTGCTGAGTGAAGACTTATCTTGAAGTTGTCAGATATGCCATAGCATGGA 528
QY 502 GTTATGATAGAGATCTCAACCTGAGAAATTTCTGTTTGTATAGTCTCTAAAGATGATGCT 561
|||
Db 529 GTGATGATCGGATCTAAAGCGCTGAGAACTTCTCTTCTGCAATAAAGAGACATCA 588
QY 562 AAGCTTAAGGTACCGATTTTGGTTTCTGCTCTCTCTATAGCCAGGACAAATATTTATAT 621
|||
Db 589 GCCCTTAAGCCATAGATTTTGGATTATFAGTCTTCTCAAGCGCTGTTGAGGATTCAC 648
QY 622 GACGTAGTTGGAAGTCCGTACTATGTTGACACAGAGGTGCTAAAGAAATTTTATGGACCT 681
|||
Db 649 GAGATTTGGAAGTCCCTTATACATGGCAGGAGGTACTTAGCCGAAATACGGACCT 708
QY 682 GAATAGATGTGGAGTGTGTTGTTTATCTCTACATTTTACTCAGCGGTTCCTCC 741

Db	709	GAGGTTGATACTGTGAGTCTCGGAGTTATCCTTTATATCCTGCTGTGTGGTGTCCACCA	768
QY	742	TTTCTGGCAGACACTGACTCGGAACTCTTAGACAGATATTGCAAGGGAAGTTAGATTTC	801
Db	769	TTTTTGGCCGAGCTGAGCAGAGGGGTGGCTCAGCGCATCAITTAGTTCAGTTATCGACTTT	828
QY	802	AAATCTGACCCGTGGCTACTACTCTCAGAAGCTGCTAAAGATTTGATCTATAAAATGCTC	861
Db	829	AAGAGGATCCATGCCGAGAGTTCTGAGACTGCCAAGACCTTGTGAGGAAGATGCTC	888
QY	862	GAAGAGGCCCAAGAACGATTTCTGCTCATGAGCGCTTGTGTACCCTATGGATGTC	921
Db	889	GAACCTGACCCCAAAAAAGCGCTTTCTGCTGCACAAGTACTCGAACATTTCTGGATACAA	948
QY	922	GATGAACAAGCAGCACCAGACAAGCTCTTGATCCAGCAGTCTTATCCTCTCTFAAGCAG	981
Db	949	AATGGAGAGAGGCTCCAAATGTTTCTCGGGGAGCGGTGAAGCAAGACTCAACAG	1008
QY	982	TTTTTCAAATGAATAAGATTAAAGAAATGGCATACGGGTAATTTGCTGAGAGACTTTCA	1041
Db	1009	TTTTTCTTATGAACAAGCTCAGAAGAGCGCTACGGGTGATAGCGAACACTTATCA	1068
QY	1042	GAGSAGAAATTGGAGGTCTGAAGGAATTGTTCAAGATGATAGACACAGACACACGGGA	1101
Db	1069	GTGGAGGAAGTAGCTGGCATCAAGGAAGCAITTGAGATGATGGACAGTAAAAAGACGGGA	1128
QY	1102	ACGATTTACTTTTCAAGAGCTCAAGCGGTTTGAAGCAGTCCGATCTGAACATGAT--G	1158
Db	1129	AAGATAACCTTCGAGGAGCTTAATTTGACTTCATAAATCGGCAGCAGCAGATACCT	1188
QY	1159	GAATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGACAACAGTGTGTAACAATAGAC	1218
Db	1189	GATACTGATCTACAGATTCTGATGGAAGTCTGATGTTGATGGGATGGGACTTTAAAT	1248
QY	1219	TACGGAGAATTCCTAGCAGCACTTTACACATGACACAGATGGAGACAGAGGAGATPCTG	1278
Db	1249	TATGGCGAGTTTGGGTGCTCTGTGTCATCTTAAGAAAAATGGCGAACGACGAACATWG	1308
QY	1279	GTGCTGCATTTTCGGACTTTGCAAGACGGAAGCGGTTATATCACCATCGATGACITT	1338
Db	1309	CATAAGGCTTTTASCTTTTTCACCAAGATCAGACGGATTCATAGAGATTGAGAGCTG	1368
QY	1339	CAGTCAGCTTGACAGA-----GTTTGTCTATGTGATACACCTCTCGGACGACATGATC	1392
Db	1369	CGTAGGCTTTAAATGATGAGGTGGATFACTACAGTGAAGAAGTTGTTGCAGCTATTATG	1428
QY	1393	AAGGAGATGTGATTTGACAATGACGGGAAGATCGATTTCTCGGAGTTTTCAGCAATGATG	1452
Db	1429	CAAGATGTTACACAGACAGGACGACGAGCGAATAAGCTATGAAGAGTTTTCGGCGCATGATG	1488
QY	1453	A 1453	
Db	1489	A 1489	

RESULT 9

US-09-988-462-20 ; Sequence 20, Application US/09988462 ; Publication No. US20030046726A1

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lytle D.
Wright, Martha S.
Merlin, Ellis J.
Mauniss, Karen L.

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in Figure 30."
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-988-462-20

Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

QY	590	CTGCTCTCTAATAGCCAGGACAAATATTTATACGCTAGTTGGAACTGCGCTACTATGTTG	649
Db	301	CCGCTCTCTTCAAGAGGAGCGAGCTGCTCAGGAGACATCGTCGGCAGCGCTACTACATCG	360
QY	650	CACCAGAGGTGCTAAAGAAATTTATGGACCTGAAATAGATGTGTGGAGTCTGCTGGTTA	709
Db	361	CGCCCGAGGTGCTCAAGAGAAATGACGCCCGGAGCCGACATCTGGAGCGTGGCGTCA	420
QY	710	TCCTCTACATTTACTCAGCGGTTTCTCCTCCCTTCTGGGAGAGACTGAGTCTGGATCT	769
Db	421	TGCTCTACATCTTCTCGCGGCTGCTCCTCTCTGGCAGAGACGAGACGGCATCT	480
QY	770	TTAGACAGATATTCGACAGGAGNAGTTAGATTTCAAACTGACCCGTGGCTACTACTCFAG	829
Db	481	TCACCGCATCTCGGAGGCGAGCTTGACCTCTCCACGAGCCATGGCCACACATCTCGC	540
QY	830	AGCTGCTAAAGATTTGATCTATAAATGCTCGAAAGAGCCCCAAGAAACGCAATTTCTG	889
Db	541	CGGAGCGCAAGGATCTCTGTCAAGAAGATGCTCACATCAACCCCAAGGAGCGGCTCAGG	600
QY	890	CTCATGAAGCCCTTGTCACCCATCGATTTGCGATGAAACAGCAGCAGCAGCAAGCCTC	949
Db	601	CGTTCAGGTCCTCAATCACCCATGGATCAAGAAGACGGAGACGCGCTCAGCAGCGCG	660
QY	950	ITGATCCAGAGTCTTATCTCGCTTAAGCAGATTTTCTCAATGAATGAATTAAGAAA	1009
Db	661	ITGACAAAGTGTGTTCTCGACAGGCTCAAGCAGTTTCAAGGCCATGAACAGTTCAAGAAG	720
QY	1010	TGGCATTACGGTAAATTCCTGAGAGACTTCAGAGGAGAAATTTGGAGTCTGAAGGAAT	1069
Db	721	CAGCATTCAGAGATCATAGCTGGTGCCTTATCCGAGAGGAGATCACAGGCTGAAGGAGA	780
QY	1070	TGTTCAAGATGATAGACACAGACACACGCGGAACGATTACTTTTGAAGAGTCAAGCGG	1129
Db	781	TGTTCAAGAACATTCACAAAGGATAACAGCGGGACCATTAACCTTCAGCAGGCTCAAACAG	840
QY	1130	GTTTCAAGAGAGTCGGATCTGACATGATGGAATCAGAAATCAAGTCTCTCATGGATCGG	1189
Db	841	GTTTGGCAAGCAGCGGGCCACAGCTGTCAGACAGCGGAATGGAGAACTAATGGAGACAG	900
QY	1190	CTGATATCGACAAACAGTGGTACAATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACA	1249
Db	901	CTGACGCTGACGGACAGGGTTAATGACTACAGCAATTCGTCACCGCAACAGTGCATA	960
QY	1250	TGAACAAGATGGAGAGAGGAGATTCCTGGTGGCTGCATTTTCGGAGCTTTGACAAAGCG	1309
Db	961	TGAACAACATGGATAGAGAAGAGCACCTTTTACACAGCATTCAGTATTTTCGACAGGACA	1020
QY	1310	GAAGCGGTTATATCACCATCGATGAGCTTCAGTCTGACCTGACAGAGTTTGGTCTATG	1369
Db	1021	ACAGCGGGTACATTTACTAAGAAGAGCTTGAGCACGCCCTTGAAGGAGCAAGGTTCTATG	1080
QY	1370	ATACACCT--CTGGAGCAGATCATCAAGGAGATTTGATCTTGACATATGACGGAAGATCG	1426
Db	1081	ACGCCGATAAATCAAGACATCATCTCCGATGCCGACTCTGCATATGTTGAAGGATAG	1140
QY	1427	ATTTCTCGGAGTTTACAGCAATGATGAGGAAGGAGATGGAGTTGGGAGCAGAACCA	1486
Db	1141	ATTATTCAGAGTTTGTGGCGATGATGAGGAAGGAGCGGCTGGTGGCCGACCAATGAACA	1200
QY	1487	TGATGAAGA	1495
Db	1201	TCRAAGA	1209

```

1 / APPLICANT: THIELEN, NOCHA VAN
2 /
3 / APPLICANT: CHEN, ROUTING
4 /
5 / APPLICANT: SARRIA-MILLAN, RODRIGO
6 /
7 / TITLE OF INVENTION: KINASE STRESS-RELATED PROTEINS AND METHODS OF
8 /
9 / TITLE OF INVENTION: USE IN PLANTS
10 /
11 / FILE REFERENCE: 16313-0032
12 /
13 / CURRENT APPLICATION NUMBER: US/09/828,313
14 /
15 / CURRENT FILING DATE: 2001-04-06
16 /
17 / PRIOR APPLICATION NUMBER: 60/196,001
18 /
19 / PRIOR FILING DATE: 2000-04-07
20 /
21 / NUMBER OF SEQ ID NOS: 128
22 /
23 / SOFTWARE: PatentIn Ver. 2.1
24 /
25 / SEQ ID NO 13
26 /
27 / LENGTH: 1387
28 /
29 / TYPE: DNA
30 /
31 / ORGANISM: Physcomitrella patens
32 /
33 / FEATURE:
34 /
35 / NAME/KEY: modified_base
36 /
37 / LOCATION: (1385)
38 /
39 / OTHER INFORMATION: a, t, c, g, other or unknown
40 /
41 / US-09-828-313-13

```

Query Match	15.9%;	Score 277.8;	DB 10;	Length 1387;
Best Local Similarity	63.4%;	Pred. No. 3.1e-56;		
Matches	457;	Conservative	0;	Mismatches 252;
				Indels 2;
				Gaps
QY	141	TTACCTTCGGGAAAAAGACTAGGCCAAGGCCAAATTGGAACAACCTATCTCTGCACAGA	200	
DB	650	TTACATCCTGGGACGGAGCTTTGGCGAGGGCAGTTCGGAGTGACTTACCTTGTTGTA	709	
QY	201	GAATCAACCTCGCCTAAATTAGCGCTGCAAAATCGATCCGGAAGCGGAAGCTCGTGTCG	260	
DB	710	CAAGATCAACGAATGAGCGGTACGCGTGCAGAGCATCCCAAAGCGGAACCTGACCAAGTAA	769	
QY	261	CGAGGATACAGAGATGTATGCGGTGAGATTTCAGATCATGCATCTCTCTGAGCATCC	320	
DB	770	GGAGGATATCGAGAGTGTAAAGCGGAGGTTTCAGATTATGCAATCACCTGCGGGGACACC	829	
QY	321	AAATGTTGTAGGATCAAAAGGGACTTATGAAGATTTCGGTGTGTTGTTCAATATGTTATGGA	380	
DB	830	CAATATCGTGGTGTTAAAGGATGTTCGAGGACAAGCATTCGGTGCATCTGTTGATGGA	889	
QY	381	GGTTTGAAGGTGGTGAGCTTTTCATCGGATGTTTCTTAAAGTCATTTTACGTGAGCG	440	
DB	890	GCTCTGTGCAGGTGGCCAGCTCTTCGATCGCATCATGCGAAGGGGCATTTACGTGAGCG	949	
QY	441	TCAAGCTGTCAAGCTTATTAAAGAGGATCTTGTTGTTGTTGAGGCTGTGTCATTTCTCTGG	500	
DB	950	CGCGCTCCCGATATGTGCGAGTCATCGTCAATGTGGTGCACAGATGCCACTCATTAGG	1009	
QY	501	TGTTATGATAGAGATCTCAAAOCTGAGAAATTTCTTTGTTGATGTCTCTTAAAGATGATGC	560	
DB	1010	GGTCTTCCATCGGATCTCAAGCCAGAGAAATTTCTGTTGGCCAGCAAGGCTGAGGATGC	1069	
QY	561	TAAAGCTTAAGGTTACCGATTTTGGTTGTTGTTCTTCTTATTAAGCCAGGACATATTTATA	620	
DB	1070	GCTCTGAAGGCCACAGACTTCGSGTCTGCAACTTTCTTTAGCCAGGAGATGTGTTCCA	1129	
QY	621	TGAGCTAGTTGAAGTCGCTACTATGTGCACAGAGGTCCTAAAGAAATGTTATGGACC	680	
DB	1130	GGATATGTTTGGAGTGGCGTATTCAGTGGCCCTGAAGTTTGAAGAGAAGTTATGGTCC	1189	
QY	681	TGAATATAGATGTGGAGTGTGTTATTCCTCTACATTTTACTCAGCGGTGTTCTTCC	740	
DB	1190	TGAGCT-GATGTTGAGTGCAGGCGTGAATGTGTACATCTGCTGTGTGTACCCCC	1248	
QY	741	CTTCTGGGCAGAGCTAGTCTGGAATCTTTAGACAGATATTCGAAGGCAAGTTAGATTT	800	
DB	1249	CTTCTGGGCTGAAACTGASGAGGTTATCTTTGACGCTGTGCTCAAAGGGCCATAGACTT	1308	
QY	801	C-AAATCTGACCGTGGCCTACTCTCTCAGAAAGTCTCAAGAAATTTGATCTATAAAATGC	859	
DB	1309	CGAAGACGAGTCCATGGCCGAAATCTCCACAGGGGCTAGGATTTGGTGCAGGAAATGC	1368	

RESULT 10
US-09-828-313-13
; Sequence 13, Application US/09828313
; Patent No. US2002059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO D
; APPLICANT: BORNERT, HANS J.

```

QY      860 T 860
Db      1369 T 1369

RESULT 11
US-09-770-445-326/G
; Sequence 326, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Prince, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-326

Query Match      13.0%;      Score 227.4;      DB 10;      Length 955;
Best Local Similarity 61.4%;      Pred. No. 6e-46;
Matches 401;      Conservative      0;      Mismatches 246;      Indels      6;      Gaps

QY      811 CGGTGGCCTACTATCTCAGAAGCTGCTAAAGATTTCATCTATAAAATGCTCGAAAGGAGC 870
Db      955 CCATGGCCTTCTATATCTGAAGCGGAAGATCTTGTAGGAAGATGCTAACCAAGAC 896

QY      871 CCCAGAAACGGATTTCCTGCTCATGAAGCCTTGTCATCCATCGATGGATTCGATGAACAA 930
Db      895 CGGAAGAGACGAATCACGCGCTGCACAGGTTCTTGAACATCCTTTGSA---TCAAGGGGGA 839

QY      931 GCAGCACACAGACAAGCCTCTTGATCCAGCAGCTCTTATCTGCTCTAAAGCAGTTTTTCTCAA 990
Db      838 GAAGCACCAGACANGCCTATGTATAGCGCTGCTTTATCCGCAATGAAGCAATTCGAGCA 779

QY      991 ATGAATTAAGATTAAAGAAATGGCATTAACGGTTAAATTCCTGCTGAGAGACTTTTCAGAGGAGAA 1050
Db      778 ATCAACAAGCTTAAAGAAGCTAGCTCTAAAGGTTATCGCGGAGAGTCTTATCAGAGAGAGAG 719

QY      1051 ATTGGAGGCTGAAGGAATTTGTTCAAGATATAGATATAGATATAGATATAGATATAGATATAGAT 1110
Db      718 ATTAAAGGCTTTAAACCATGTTTGGCAATATAGATATAGATATAGATATAGATATAGATATAGAT 659

QY      1111 TTGGAAGAGCTCAAGCGGGGTTTTGAAGAGAGTCCGATCTCGAATCTGATGGAATCATGAATC 1170
Db      658 TATGAAGAAGCTCAAACTGGGCTTAACCTAGACTTGGGTCTAGACTCTCGGAAACTGAAGTT 599

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592 GTCTTCTATAGCCAGGACGACATATTTATATACAGCTAGTTCGAAGTCGCTACTATGTTGCA 651
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656 CCAGAGGTGCTAAAGAAATGTTATGGACCTGAAATAGATGCTGAGAGTCTGGTGTATC 711
658 CCGAGGTATTCATAGGTTATATCAATGGAAGCTGACGATGAGGATTTGGATGATC 1043
712 CTCACATTTTACACAGCGGTGTTCTCTCCCTCTGGGAGAGACTGAGTCTGGATCTTT 771
1044 ACGTACATTTTGTATGTTAGTGTAGTACCGCTTTTGGGCGCGGACCGAGTCGGGCATTTT 1103
772 AGACAGATTTGCAAGGGAAGTATGATTTCAATCTGACCGCTGGCCCTACTATCTCAGAA 831
1104 CTTGGGTGTTGAGGCTTGACCCGAGCTTTGAAGAGCCCTTGGCCCTTCCATCTCTCCC 1163
832 GCTGCTAAAGATTTGATCTATAAATGCTCGAAGAGGCCGCCAAGAAAGCAATTTCTGCT 891
1164 GAAGCAAGGATTTCTGTAAGGCTCTCTGTAAGATAGGATATGCGGAACGCGATGACTGCT 1223
892 CATGAGCTTGTCTACACCATGATTTGCGATGAACAGAGCACCACAGCCTCTTT 951
1224 GCACAAGCTTTAACTCATCTCATGATTCGAAGTAAACAAG-----TGAAGATACCTCTG 1277
952 GATCCAGCAGCTTATCTGCTCTAAAGCAGTTTCTCAAATGAATAAGATTAAAGAAATG 1011
1278 GATCTTAGTGTACAGACTTGTGAGGATTTATCTGTCATCATCTCAGAAAGGCT 1337
1012 GCATTACGGGTAAATGCTGAGAGACTTTCAGAGGAGAAATTTGGAGTCTGAAGGAATG 1071
1338 GCTTTGAGGCGCTGTCAAAGACTTTAACCGAAGACGAGACTTTTATCTAGTACTCAA 1397
1072 TTCAGATGATACACACACACAGCAGCGAAGCAATTTTGAAGAGCTCAAAGCGGT 1131
1398 TTTATGCTGCTAGCAAGTAAACAGCTGTGTTGTTTACTTTTGTAGAAATTCACACAGGCA 1457
1132 TTGAGAGAGTCTGGATCTGAATGATGAA 1161
1458 CTGCTGAANAATTCACAGAGGCGCATGAAA 1487

RESULT 13
US-09-988-462-26
; Sequence 26, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Kyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
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NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-988-462-26

ORGANISM: Arabidopsis thaliana
US-09-938-842A-1063
Query Match 11.5%; Score 200.6; DB 9; Length 1800;
Best Local Similarity 52.4%; Pred. No. 3.4e-39;
Matches 490; Conservative 0; Mismatches 439; Indels 6; Gaps 2;
QY 229 RAATCGATCCCGAAGCGTCTGTCGCGAGGATTCGAGAGATGTATGGCGTGAAG 288
DB 526 AAAGTCATCCCAAAATCTAAGATGACATCTGCAATATCTATAGAGATGTGAGAGAGAA 585
QY 289 ATTCAGATCATCATCATCTCTCTGAGCATCCAAATGTTTGGTATGAGTCAAGGACCTAT 348
DB 586 GTGAAAATCTCGGCGCTTATCTGACATCAAAATTTGTTACAAATTTCTATGATCGGTTT 645
QY 349 GAAGATTCGGTGTGTTTTCATATTTTATGAGGTTTGTGAAGTGTGAGTGTGTTTGTAT 408
DB 646 GAGGACAATSCCAACGTTTACATCGTTATGAGGATTTATGAGGAGTGTGAGTGTGTTGAC 705
QY 409 CGGATGTTTCTA--AAGGTCTATTTAGTGAGCGTGAAGCTGTCAAGCTTTAAGAGCG 465
DB 706 AGGATCTAGCAGGAGGAGAAATCTCTGAAGATGATCAAAAGCAGTGTCTTATACAG 765
QY 466 ATTCCTTGGTGTGTTGAGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 525
DB 766 ATCCCTTAACGTCTAGCTTCT 825
QY 526 GAGAAATCTCTGTTTGTATAGTCTCTAAAGATGATGCTTAAAGCTTAAAGCTTAAAGCT 585
DB 826 GAGAAATCTCTGTTTGTATAGTCTCTAAAGATGATGCTTAAAGCTTAAAGCTTAAAGCT 885
QY 586 TTGCT 645
DB 886 TTATCGGACCTTGTCTAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
QY 646 GTTGCCACAGAGGCTTAAAGAAATGTTTGGACCTCAAAATAGATGTGTGGAGTGTGTGT 705
DB 946 GTAGCCCTTGAAGTCTTACACAGATCTTATACACAGAGGAGGAGGAGGAGGAGGAGGAG 1005
QY 706 GTTATCT 765
DB 1006 GTCATAGCATACATCT 1065
QY 766 ATCTTTAGACAGATTTGCAAGGAGGAGTGTATGATTTCAAACTGACCGTGTGCTTACATC 825
DB 1066 ATTTTTCAGAGCAGTCTTAAAGCTGATCCCACTTTTGTATGAACCTCTCTGCTCTCTCT 1125
QY 826 TCAGAGCTGTAAAGATTTTGTATCTATATAATGCTCAAGAGGAGGAGGAGGAGGAGGAGG 885
DB 1126 TCCCTTGAAGGCAAAAGATTTTGTATGAGATTTATGTTACAGGAGGAGGAGGAGGAGGAG 1185
QY 886 TCTGCTCATGAAGCTTGTGTCACCCATGGATTTGATGATGATGATGATGATGATGATGAT 945
DB 1186 ACTGCATCTCAAGCTTGTATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1242
QY 946 CCTCTGTATCCAGCAGTCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1005
DB 1243 CCATTGTATTTCTGATCTTCAAGCAGATCAAGAGCATCTTGTGATCTTGTCTCTCTCTCT 1302
QY 1006 AAAATGGCATACGGTAAATCTCTGAGAGCTTTTTCAGAGGAGGAGGAGGAGGAGGAGG 1065
DB 1303 AAAGCTGCTTGTATGCTCTGTCACAGCATTAACCTACCGATGATCACTCTCTCTCTCTCT 1362
QY 1066 GAATTTTCAAGATGATGACACAGACAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1125
DB 1363 GCGCAGTTTGCACACTTAGACGCAACAAATGGCCCTCATCACTTTAGATAGCATCAGA 1422
QY 1126 GCGGCTTTGAAGAGAGTCTGGATCTGAACGTGATGA 1160
DB 1423 CTGGCAGCTTGGCAGAAATCAACAGAGCAATGAA 1457
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Query Match 12.5%; Score 218; DB 9; Length 4162;
Best Local Similarity 59.8%; Pred. No. 2.9e-43;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 142 TACCTTCGCGGAAAAAGCTAGGCAAGGCGAATTTTGAACAACCTATCTCTGACAGAG 201
DB 1757 TACTCGATGGCAAGAGCTCGGCGCGGAGTTCGCGGTGACACACTGTGACGCGAC 1816
QY 202 AAATCAACCTCCGCTANTTACCCCTGCAATCGATCCCGAAGCGGAGGAGGAGGAGGAGG 261
DB 1817 CGGACGAGGCGGAGAGCTGGCTGTCAGAGAGATCGGAGCGGAGGAGGAGGAGGAGG 1876
QY 262 GAGGATTTAGAGATCAAGAGGACTTATGAAGATCGGTGTTTGTATATGTTATGAGG 381
DB 1877 GAGGAGCTGAGACGCTGCGGCGGAGGAGTGCAGATCATGCAACCACTCTCCGCGCAGCC 1936
QY 322 ATGTTGTAGATCAAGAGGACTTATGAAGATCGGTGTTTGTATATGTTATGAGG 381
DB 1937 AAGCTGTGCGGCTCGGCGCGGCTACGAGGAGCAAGCAGGCTGCACTCGICATGGAG 1996
QY 382 GTTGTGAGGTGCTGAGCTTTTGTATCGGATTTGTTCTAAAGGTCAATTTAGTGAAGCT 441
DB 1997 CTGTGCGGCGGAGAGCTTTCGACCGCATCAICGCGGCGGAGTACACGAGCGC 2056
QY 442 GAAGCTGTCAAGCTTATTAAGACAGATCTTGTGTTGTTGAGGCTTGTCTATCTCTGTT 501
DB 2057 GCGCGCGGAGCTGCTGCGGCGCATGTCAGATCGTGCACACCTGCCACTCCATGGGG 2116
QY 502 GTTATGATAGATCTCAACCTGAGAAATTTCTGTTGATAGTCTTAAAGATGATGCT 561
DB 2117 GTGATGACCGGAGACATCAAGCGGAGAACTTCTGCTGCTCAGCAGGAGGAGGAGCGG 2176
QY 562 AAGCTTAAAGCTACCGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 621
DB 2177 CCGCTCAAGGCCACCGACTTCGCGCTCTCGCTCTCTCTCAAGGAGGCGAGCTCTCAGG 2236
QY 622 GACGTAGTTGAAGTCTGCTACTTGTTCACAGAGGCTGTAAAGAAATGTTATGAGACT 681
DB 2237 GACATCTGCGCAGCGGCTACTGATCGGCGCGAGTGTCTCAAGAGGAGTACGCGCGG 2296
QY 682 GAAATAGATGTTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 741
DB 2297 GAGCGCGACATCTGAGGCGTGGGCTGCGGCTGATGCTTACATCTTCTCTCGCGGCGTCC 2356
QY 742 TCTGCGGAG 751
DB 2357 TCTGCGGAG 2366
RESULT 14
US-09-938-842A-1063
Sequence 1063, Application US/0993842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepis, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1063
LENGTH: 1800
TYPE: DNA

US-09-938-842A-3678
; Sequence 3678, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3678
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3678

Query Match 11.0%; Score 193; DB 9; Length 718;
Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CTCATCATCTTCCACAAATTCGTTTTTCTCTTTAAATTCGTTATATTTGAATT 60
QY 1615 CTAATTTCTAGGATACAAAATATATCTGGCTTGTTTTTCTCTTTATTTT 1674
DB 61 CTAATTTCTAGGATACAAAATATATCTGGCTTGTTTTTCTCTTTATTTT 120
QY 1675 GTACATGAGCAACTTCTAAATTTTATCCCTCATATGATAATTTTGCCTTCATATAAA 1734
DB 121 GTACATGAGCAACTTCTAAATTTTATCCCTCATATGATAATTTTGCCTTCATATAAA 180
QY 1735 GTTTTGAATCC 1747
DB 181 GTTTTGAATCC 193

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Job time : 513 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 23:20:21 ; Search time 3002 seconds

(without alignments)
9424.889 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743375 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_othr.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	598	34.2	2380	11	AY109473
2	563.4	32.2	591	10	AV825282
3	523.6	30.0	2566	11	AY109374
4	505.8	29.0	2298	11	AY109401
5	503.8	28.8	507	10	AV558412
6	484	27.7	835	12	BG647837

C	7	480.6	27.5	1628	11	AY109463
	8	466.8	26.7	814	12	BG887873
C	9	439	25.1	493	17	B28263
C	10	437.8	25.1	1087	17	B11596
	11	424.8	24.3	528	9	AI994248
	12	418	23.9	742	12	BG596613
	13	402.4	23.0	813	14	BM779035
	14	401.8	23.0	686	13	B1178776
	15	388.8	22.3	751	14	BQ865474
	16	379.2	21.7	723	14	BQ986998
	17	375.8	21.5	635	10	AW587489
	18	374.2	21.4	695	14	BQ115699
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	20	374	21.4	777	14	BQ990883
	21	372.6	21.3	689	14	BQ506885
	22	371.4	21.3	697	13	BQ302783
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	25	355.2	20.3	727	14	BQ765967
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	28	351.6	20.1	635	10	AW011661
	29	347.6	19.9	683	14	BU005844
	30	347	19.9	748	14	BQ967112
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	32	342.8	19.6	700	9	AI506058
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	36	339.8	19.5	747	14	BQ970309
	37	338.2	19.4	635	10	AV925405
	38	335.2	19.2	673	14	BQ865634
	39	331	18.9	612	13	B1074799
	40	330.4	18.9	564	9	AI894480
	41	329.4	18.9	740	12	BG238387
	42	324	18.5	682	13	BJ292898
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	45	322.4	18.5	658	10	AV914419

ALIGNMENTS

RESULT 1
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LOCUS AY109473 2380 bp linear HTC 25-MAY-2002
DEFINITION Zea mays CL1905_1 mRNA sequence.
ACCESSION AY109473
VERSION AY109473.1 GI:21213206
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.

TITLE
Maize Mapping Project/Dupont Consensus Sequences for Design of

JOURNAL
REFERENCE
AUTHORS
Overgo Probes
Unpublished (2002)

TITLE
Direct Submission
Coe,E.C.

JOURNAL
REFERENCE
AUTHORS
Submitted (25-APR-2002) Maize Mapping Project, University of

TITLE
Missouri, Columbia, MO 65211, USA

FEATURES
Location/Qualifiers
1..2380

Source
/organism="Zea mays"
/db_xref="MaizeDB:630571"
/db_xref="taxon:4577"
/clone="CL1905_1"

BASE COUNT	478 a	560 c	507 g	468 t	367 others
ORIGIN					

Query Match	34.2%	Score 598	DB 11	Length 2380
Best Local Similarity	60.7%	Pred. No. 1.5e-99		
Matches 859	Conservative	0	Mismatches 557	Indels 0
QY	104	CAGTCTTACCATATCAAAACACCACGATTAAGAGATCAATTACCTTCTGGGAAAAAGCTAG	163	
DB	589	CCGTGCTCNN	648	
QY	164	GCCAAAGSCCAATTGGGAACAACTTATCTGTCACAGAGAATCAACCTCCGCTAATTACG	223	
DB	649	GGCAGGGGCAGTTCGGACCAACCTTCTCTGCACCGAGCTGCCACGGGATCGACTACG	708	
QY	224	CCTCAATCGATCCCGAAGCGAAGCTCGTGTGCGGAGGATTCACGAAGATGTATGGC	283	
DB	709	CCTCGAGTCCATCTCCAAAGCGAAGCTCATCACAGGAGGACGCTGACGACGTGCGCC	768	
QY	284	GTGAGATTCAGATCATGATCATCTCTGAGCATCCAAATGTTGTAGGATCAAGGGA	343	
DB	769	CGAGATCCAGATCATGACCAACCTCTCGGCGCACCAACGCTCGCGCATCAAGGGCG	828	
QY	344	CTTATGAAGATTCGGTGTGTTGTCATATGTTATGAGGTTTGTGAAGGTGTGAGCTTT	403	
DB	829	CCTACGAGACACAGCTCTACGTCACATCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	888	
QY	404	TTGATCGGATCTTTTCTAAAGTGCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAGA	463	
DB	889	NNNNNNNNNNNACAGCGCGCACTACAGCGAGGCAAGCGCGCGGCTCACAGGA	948	
QY	464	CGATTCCTGGTGTGTTGAGGCTTGTCACTCTCTGTTGTATGATAGAGATCTCAAAAC	523	
DB	949	TCATGTGCGGCTGTCGAGCGTGCACCTCCCTCGGGGTTCATGCACCGGAGCTCAAGC	1008	
QY	524	CTGAGAAATTCCTGTTTGATAGTCTTAAAGATCATGCTAAGCTTAAGGCTACCGATTTG	583	
DB	1009	CCGAGAACTTCCTGCTGCGCCACAGGACGATGACCTCTCGCTCAAGGCCATGATTCG	1068	
QY	584	GTTTGTCTGCTTCTATAAGCCAGGACAATTTATATGACGTAGTTGGAGTCCGTA	643	
DB	1069	GACTCTGTCTTCTCAAGSCCTGGTCAAGTTTCAACGATGTTGTTGGTAGCCCATAT	1128	
QY	644	ATGTGACACAGAGGCTCTAAGAAATTTATGACCTGAATAGATGTGGAGTGGTG	703	
DB	1129	ATGTAGTCCAGAAATTTTGTGAAAAGTTATGGACCAAGCAGCTGATGATGACAGCTG	1188	
QY	704	GTGTTATCTCTACATTTTACTCAGCGTGTTCCTCCTCTGGCAGAGACTGAGCTG	763	
DB	1189	GTGTCATCTTTACATCTACTGAGTGTGTGCTCCATTTTGGCAGAAAACACAACAG	1248	
QY	764	GAATCTTTAGACAGATTCGAAGGAAGTTAGATTTCAATCTGACCCGTGGCCTACTA	823	
DB	1249	GAATATTTGATGCTGTAATGAAGGGTGCCATGATTTTGTATCTCATCCGTGGCCTGCA	1308	
QY	824	TCTCAGAAGCTGCTAAAAGATTTGATCTATAAATGCTCGAAAGGAGCCCAAGAACGCA	883	
DB	1309	TATCTGATAGTGCAAAAGATCTTATCAGACGAATGCTGAATCCTGCTCTGCCGAGCT	1368	
QY	884	TTTCTGCTCATGAAGCCTTGTGTCACCATGATGATGTCGATGAACAAGCAGACCCAGCA	943	
DB	1369	TAAACAGCATGAAGTTTCTATGCCATCCATGATGATGCTGATCATGAGTAGCTCTGACC	1428	
QY	944	AGCCTCTTGATCCAGCAGCTCTTATCTCGCTTAAAGCAGTTTCTCAATGAATGAATTA	1503	

1429 GTCCACTGGATCCAGCTGCTTATCTCGCATTAAAGCAATTCCTGCAATGAATAGTTGA 1488

1004 AGAAATGGCATACGGGTAAATTCCTGAGACACUUTTCAGAGGAAGAATTCGGAGGTCTGA 1063

1489 AGAAATGGCTTTACGAGTAATAGCTGAGAGCCTATCAGAAGAGAAATTCGGGGTTGA 1548

1064 AGGAATGTTCAAGATGATAGACACAGACACACAGCGGAACGATTACTTTGAAGAGCTCA 1123

1549 AGAAATGTTCCAGACCATGGACATGCACAGTGGCGCAATTACTTATGATGAGCINN 1608

1124 AAGCGGGTTTGAAGAGAGTCGGAATCGAAGTATCAGAATCAAGTCTCTCATGG 1183

1609 NNNNNNNNNNNNNNNNGGCTCCACCTAAAGGACACTGAGATTCGTGATCTTATGG 1668

1184 ATCGGCTGATATCGACACACAGTGGTACAAATAGACTACGGAGAATTCCTACGACACACT 1243

1669 ATGCACTGATATGTGACACAGTGGAAACAAATTCGACTACATAGAAATCAATTCGCAACT 1728

1244 TACACATGAACAAGATGGAGAGAGAGATTCCTGGTGGCTGCATTTTCGGACTTTGACA 1303

1729 TGCATCFCAATAGCTGGAGCGTGAAGACATCTCGTGGCAGCCTTTTCATATTTGCGACA 1788

1304 AAGCGGAAGCGGTTATATACCATCGATGAGCTTCAGTCAGTCGACAGAGTTTGGTC 1363

1789 AAGATGTAGTGGCTATATCACAGTGGACGAACATACAGAACTTCGAANGAGCAATACA 1848

1364 TATGTGATACACCTCTGGACGACATGATCAAGGAGATTCATCTTGACAAATGACGGGAAGA 1423

1849 TGCCGGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGATCAGGATAACGATGGCCGCA 1908

1424 TCGATTTCTCGAGTTTACAGCAATGATGAGGAAGAGAGATGGAGTTGGGAGNAGCAGAA 1483

1909 TTGACTATGGAGATGTTGTCCTCATGATGACCAAGGCAATATGGGATCGGTGCGAAGAA 1968

1484 CCATGATGAAGAACTTGAACTTCACATTCCTGATG 1519

1969 CAATGAGAAACAGCTTGAATATCAGATCAGAGGACG 2004

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AV825282	RAFL7	Arabidopsis thaliana CDNA clone RAFL07-07-K16 5', mRNA	591 bp	linear	EST 01-APR-2002		
AV825282	RAFL7	Arabidopsis thaliana CDNA clone RAFL07-07-K16 5', mRNA sequence.					
AV825282							
AV825282.1	GI:19867342						
EST							
thale cress.							
Arabidopsis thaliana							
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliopsida II; Brassicales; Brassicaceae; Arabidopsi.							
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.							
1 (bases 1 to 591)							
Seki.M., Narusaka.M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono.Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.							
Reference							
Authors							
Shinozaki,K.							
Arabidopsis full-length cDNA (2002b)							

Large scale analysis of Arabidopsis full-length cDNA (2002b)
TITLE
JOURNAL
COMMENT
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified paluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

TITLE		Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes	
JOURNAL		Unpublished (2002)	
REFERENCE		2 (bases 1 to 2566)	
AUTHORS		Coe,E.C.	
TITLE		Direct Submission	
JOURNAL		Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	
FEATURES		Location/Qualifiers	
source		1..2566	
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		/clone_lib="Maize Mapping Project/DuPont Consensus Library"	
		/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."	
BASE COUNT	440 a	680 c	777 g
ORIGIN	420 t	249 others	
Query Match 30.0%; Score 523.6; DB 11; Length 2566;			
Best Local Similarity 60.2%; Pred. No. 5.4e-86;			
Matches 799; Conservative 0; Mismatches 528; Indels 0; Gaps 0;			
QY	131	TAAGAGATCATTTACCTTCTGGGAAAAAGCTAGCCAAAGCCAAATTTGGAACAACCTATC	190
DB	758	TCRAGGACAAAGTACNN	

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/organism="zea mays"
/db_xref="MaizeDB:630430"
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Library"
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assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
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BASE COUNT	544 a	464 c	597 g	524 t	169 others
ORIGIN	Mapping project				
Query Match	29.0%; Score 505.8; DB 11; Length 2298;				
Best Local Similarity	61.8%; Pred. No. 9.9e-83;				
Matches 817; Conservative	0; Mismatches 502; Indels 3; Gaps				
QY	142	TACTCTCTGGGAAAAAGCTAGCCACGAGCCAAATTGGACAAACCTATCTCTGCACAGAG	201		
DB	666	TACTCCCTCGGGAAGGAGCTTGGCCGGGCGAGTTCGGGTGACATACCTCTGCACAGAG	725		
QY	202	AAATCAACCTCCCTTAATTACCCCTGCAAATTCGATCCCGAAGCGAAAGCTCGTGTCTGCGC	261		
DB	726	GTTCGCTCTGGGAGGAGCAGTACGCCCTGCAAGTCCATCTCCAAGCGCAAGCTCGCCAGCAAG	785		
QY	262	GAGGATTCAGAAGATGATGGCGTCAGATTCCAGATCATGCAATCATCTCTGAGCATPCA	321		
DB	786	GCAGACAGGAGGAGCAATTCGAGGGAGATCCAGATCATGAGCACCTGTCTGGCAGCCCA	845		
QY	322	AAATGTTGTTAGGATCAAAAGGAGCTTATGAAGATTCGGTGTGTTGTTCTCATATGTTATGGAG	381		
DB	846	AACATTTCTCAGTTCCGGGAGCATACGAGGACAAGCAATGTCCATGTGGTATGGAG	905		
QY	382	GTTTGTGAAGGTGGTGAGCTTTTGTATCGGATGTGTTTCTAAAGTCAATTTTATGAGCGT	441		
DB	906	CTCTGCGCAGGTGGGAGCTCTTCGATCGCATCATGTCGAAGGGGCACTACACAGACGT	965		
QY	442	GAACTCTCAAGCTTATTAAGACGATTCCTGGTGTGTTGTAGGCTTGTCATTCCTTGGT	501		
DB	966	CGGCTGCTCAATCTCAGAGCAGTGTGATGTGTGATGTGTGCACATTTGCCATTCATGGT	1025		
QY	502	GTATGCATAGAGATCTCAACCTCGAATTTCTTGTGTTGATGTCCTAAAGATGATGCT	561		
DB	1026	GTATGCACCGTGACCTGAAACCGGAGAACTCTTCTGCGACGACGAGGAGAGATGCA	1085		
QY	562	AGCTTAAGGCTACCGATTTTGGTTGTCGTCTCTATAAAGCCAGGACAAATTTATAT	621		
DB	1086	ATGCTCAAGGCCACTGATTTGGGCTTTTCGCTTTCATCGAAGAGAAAGATGTACAGG	1145		
QY	622	GACCTAGTTGGAAGTCGCTACTATGTGACACGAGGCTGCTAAAGAAATGTTATGGACCT	681		
DB	1146	GACATCGTTGGAATGCTTATATGTGCGCTGAAGTCTCTTAAGCGGAGCTATGGAAA	1205		
QY	682	GAATAGATGTGTGGAGTGTGTTGTTATCCTCTACATTTTACTCAGCGGTGTTCCCTCC	741		
DB	1206	GASATAGATGTTGGAGCGCAGGTGTTATTTGTACATTTCTCAGTGGTGTGCTCTCA	1265		
QY	742	TTCCTGGGACAGACTGAGCTGTGGAATCTTTAGACAGATATTCGAAGGAAAGTATGATTC	801		
DB	1266	TTTTGGGCTGAAATTTGAAAGGGGATATTTGATGCTATTTCTGATGAGGAGATTCAC	1325		
QY	802	AAATCTGACCGTGGCCTACTATCTCAGAAGCTGAAGATTTGATCTATAAAATGCTC	861		
DB	1326	GAAAGTCAACCTTGCCCATCAATTTCTGAGAGTGTCTAAAGCTTGTTTGAAGATGTG	1385		
QY	862	GAAGAGGCCCAAGAAAGCAATTTCTGCTCATGAAGCCCTGTGTCAACCCATGGATGTC	921		
DB	1386	ACACGAGATCCAAAGAAAGAAAGACTGACTTCAGCTCAAGTTCTTCAACATTCATGGCT	1445		
QY	922	GATGAACAAGCAGCACAGCAAGCCTCTTGATCCAGCAGCTTATCTGTGCTTAAGCAG	981		

RESULT	4
LOCUS	AY109401
DEFINITION	Zea mays CL1577_1 mRNA sequence.
ACCESSION	AY109401
VERSION	AY109401.1 GI:21213112
KEYWORDS	HTC.
SOURCE	Zea mays.
ORGANISM	Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 2298) Hainey,C.F., Dolan,M., Miao G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes Unpublished (2002) 2 (bases 1 to 2298) Coe,E.C. Direct Submission Submitted (25-APR-2002) Maize Mapping Project, University of, Missouri, Columbia, MO 65211, USA Location/Qualifiers
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	

/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT	179 a	104 c	80 g	144 t				
ORIGIN								
Query Match	28.8%; Score 503.8; DB 10; Length 507;							
Best Local Similarity	99.6%; Pred. No. 3.6e-82;							
Matches 505; Conservative	0; Mismatches 2; Indels 0; Gaps 0;							
QY	1241	CCCTACACATGAACAAGATGGAGAGAGAGAGATCTCTGGTGGTGCATTTTCGGACACTTTG	1300					
Db	507	CCCTACACATGAACAAGATGGAGAGAGAGAGATCTCTGGTGGTGCATTTTCGGACACTTTG	448					
QY	1301	ACAAAGACGGAAGGGTTTATATACCATTCAGCTTCAGTCAGCTTCAGCAGAGTTTG	1360					
Db	447	ACAAAGACGGAAGGGTTTATATACCATTCAGCTTCAGTCAGCTTCAGCAGAGTTTG	388					
QY	1361	GTCTATCTGATACACCTCTGGACGACATGATCAAGAGAGATGATCTTGCACAAATGACGGGA	1420					
Db	387	GTCTATCTGATACACCTCTGGACGACATGATCAAGAGAGATGATCTTGCACAAATGACGGGA	328					
QY	1421	AGATCGATTTCTCGGAGTTTACACCAATGATGAGAAAGGAGATGGAGTTGGGAGAGCA	1480					
Db	327	AGATCGATTTCTCGGAGTTTACACCAATGATGAGAAAGGAGATGGAGTTGGGAGAGCA	268					
QY	1481	GAACCATGATGAAGAATCTGACATTCACATTCGATGCTTTGGAGTTGATGCTTAAATTCGT	1540					
Db	267	GAACCATGATGAAGAATCTGACATTCACATTCGATGCTTTGGAGTTGATGCTTAAATTCGT	208					
QY	1541	AATCTGATGACTGACTCATCTTCCACAAATTCCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTT	1600					
Db	207	AATCTGATGACTGACTCATCTTCCACAAATTCCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTT	148					
QY	1601	TTATATTTTGAATCTTAATTTCTTAAAGATACAAAATATATCTGCTTTGCTTTTCTTTTCTTTT	1660					
Db	147	TTATATTTTGAATCTTAATTTCTTAAAGATACAAAATATATCTGCTTTGCTTTTCTTTTCTTTT	88					
QY	1661	TCCTTTTATTTTGTACATGAGCAACTTCTTAAATTTTATCCCATATGATGATATTTT	1720					
Db	87	TCCTTTTATTTTGTACATGAGCAACTTCTTAAATTTTATCCCATATGATGATATTTT	28					
QY	1721	TGCTTCATATATAAGTTTTTGAATTC	1747					
Db	27	TGCTTCATATATAAGTTTTTGAATTC	1					
RESULT 6								
LOCUS	BG647837	835 bp	linear	EST 24-APR-2001				
DEFINITION	EST509456 HOGA Medicago truncatula cDNA clone phoga-18E5 5' end,							
ACCESSION	BG647837	Medicago truncatula						
VERSION	BG647837.1	GI:13782949						
KEYWORDS	EST.							
SOURCE	barrel medic.							
ORGANISM	Medicago truncatula							
REFERENCE	1 (bases 1 to 835)							
AUTHORS	Hahn, M.G., O'Janen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,							
TITLE	ESTs from roots of Medicago truncatula treated with							
JOURNAL	oligogalacturonides of DP 6-20							
COMMENT	Unpublished (2001) Contact: Michael G. Hahn Complex Carbohydrate Research Center University of Georgia 220 Riverbend Road, Athens, GA 30602-4712, USA Tel: 706-542-4457 Fax: 706-542-4412 Email: hahn@ccrc.uga.edu							

G391443e TIGR sequence name: MTNCE27TK More information is available at: www.medicago.org
 Seg primer: SKmod (CTA qAA CTA qtg qAT CC).

FEATURES

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/lab_host="XLOLR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in SOLR cells."
230 a 137 c 210 g 258 t
BASE COUNT

```

BASE COUNT	230 a	137 c	210 g	258 t
ORIGIN				
Query Match		27.7%	Score 484;	DB 12; Length 835;
Best Local Similarity		75.2%;	Pred. No. 1.3e-78;	
Matches 629;	Conservative	0;	Mismatches 205;	Indels 2; Gaps 2;

Qy	406	GATCGGATGTTCTC	AAAGTCATTTT	TAGAGCGTGAAGCTGT	CAAGCTTATT	AAAGACG	466
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Qy	466	ATTCCTGGGTGTTG	TGAGGCTTGT	CATCTCTCTGGTTAT	GCATAGAGATCT	CAAACT	525
Db	62	ATTCCTGAGGTGT	TGAAGCTTG	CACTCTCTGGAGTTAT	TGCACAGACCTT	TAACCT	121
Qy	526	GAGAAATTCCTGTT	TGATAGCTCT	AAAGATGAT	CTAAAGCTT	TAAGCTACCCGATTTTGGT	585
Db	122	GAGAAATTTTGT	TGATCTGTTG	TATGAAGATGCTCT	TCTCAAACTAT	TGATTTTGGT	181
Qy	586	TGTGCTGCTCT	CTATAAGCCAGGAC	CAATATTTATATGACGTAGT	TTCGAGTCCG	TACTAT	645
Db	182	TGTGCTGTGTTTT	TACAAGCCAGGTGA	AACTCTTTAGTGATGTTGTT	TGGAAGCCCTACTAT		241
Qy	646	GTTCACACAGAGT	GTCTAAAGAAATGT	TATGGACCTGAAATAGAT	GTGTGGAGTGTGCTGT		705
Db	242	GTTCGCCAGAGG	CTTTGCACAAACAT	TATGGACCTGAAGCAGCTGT	TGGAGTGTGCTGT		301
Qy	706	GTTATCTCTCAT	TTTTACTCAGGGTGTTCT	CTCCCTCTGGGCACAGACT	GAGTCTGGA		765
Db	302	GTATTTTGTACAT	CTCTATTAAAGCGGGTGCTCCGCTTTT	TGGCCGAGACCGCATCAAGGG			361
Qy	766	ATCTTTAGACAGAT	TTCGAAGGCAAGTTAGATTTCAAACT	CTGACCGCTGGCTCTACTATC			825
Db	362	ATCTTACAGACAGAT	TTTTCCAAAGGAAACCTTGATTTCCGCTCT	GAGCGCTGGCTCGGAT			421
Qy	826	TCAGAAGCTGCT	TAAGATTTTGATCTAT	AAAAATGCTGAAAGGAGCCCCAAGAAACGCAT			885
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QY	1126	GCGGTTTGAAGAGAGTCGGATCTGAACATCAAGAAATCAGAANAATCAAGTCTCTCATGGAT	1185
Db	722	GAAAGCCTTAAAGCCAGTAGGATCTGAACCTTATGGAGCTCG-AATCAAGAGATCTTATGGAT	780
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Db	781	CAGCAGATATAGATTATA-CGGACACACTTGACTATGGCAATTCATTGGTGTGAC	835

RESULT 7

AY109463/C	AY109463	1628 bp	linear	HTC 25-MAY-2002
LOCUS	CL10776_2	mrna		
DEFINITION	zebra mays			
ACCESSION	AY109463			
VERSION	AY109463.1			
KEYWORDS	HTC			
SOURCE	zebra mays			
ORGANISM	zebra mays			

RECEIVED

REFERENCE 1 (bases 1 to 1628)
AUTHORS Halney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgance, M. and Ringey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1628)
AUTHORS Coe, E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES Location/Qualifiers

FEATURES

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overgo addressing of BACs in conjunction with the Maize
Mapping Project"

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BASE COUNT	393 a	408 c	350 g	424 t	53 others
ORIGIN	Mapping Project				

Query Match	27.5%;	Score 480.6;	DB 11;	Length 1628;
Best Local Similarity	60.0%;	Pred. No. 4.3e-78;		
Matches 775: Conservative	0;	Mismatches 514;	Indels 3;	Gaps 1;

[illegible]

RESULT #	LOCUS	DEFINITION	814 bp	mRNA	linear	EST 30-MAY-2001
8	BG887873	EST513724 cSTD Solanum tuberosum cDNA clone cSTD7P13 5' sequence, mRNA sequence.				
ACCESSION	BG887873					
VERSION	BG887873.1	GI:14264959				
KEYWORDS	EST.					
SOURCE	potato.					
ORGANISM	Solanum tuberosum					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.					
AUTHORS	1 (bases 1 to 814)					
TITLE	van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemiango,A., Bougri,O., Buel,C.R., Ronning,C., Tanksley,S. and Baker,B.					
JOURNAL	Generations of ESTs from dormant potato tubers					
COMMENT	Unpublished (2001) Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com					
FEATURES	Seq primer: M13P-R.					
source	Location/Qualifiers					
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	/tissue_type="dormant tuber"					
	/dev_stage="one month post-harvest"					
	/lab_host="SOLR"					
	/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."					
BASE COUNT	242 a 146 c 191 g 235 t					
ORIGIN						
Query Match	26.7%; Score 466.8; DB 12; Length 814;					
Best Local Similarity	73.3%; Pred. No. 1.8e-75;					
Matches	597; Conservative 0; Mismatches 217; Indels 0; Gaps 0;					
QY	438 CGGTGAAGCTGTCAAGCTTATTAGACGATCTCTGGTGTCTTGAGGCTTGTCATTCTCT	497				
DB	1 GAGAAAGCTGCACAAATTGATGAAACATATTGTCAAGTTCTGGAGGCTTGTCATTCTCT	60				
QY	438 TGGTGTATTGATAGATAGATCTCAACCTCGAATTTCTTTGTTGATAGTCTTAAGATGA	557				
DB	61 TGGGTTTATGATAGATAGATCTCAACCTCGAATTTCTTTTGTGATAGTCTGATGAAGA	120				
QY	558 TGCTAAGCTTAAAGGCTACCGATTTTGGTTTGTCTGTCTCTATAGCCAGGACAAATATT	617				
DB	121 TGCTAAGCTTAAAGGCTACTGATTTTGGTCTCTCTATTTCTATAGCCAGGACAAAT	180				
QY	618 ATATGACGTAGTTGGAAGTCCGTACTATGTTGACACGAGGTGCTTAAGAAATGTTATGG	677				
DB	181 CTCAGATGTTGTTGGAAGTCCATATATATGTTGCTCCTCAAGTTGTGCAACAATACTATGG	240				
QY	678 ACCTGAATAGATGTTGAGGAGTGGTGTATCTCTCTACATTTTACTCAGGGGTGTCC	737				
DB	241 GCGTGAATAGACGTCTGAGTGTGGAGTCACTCTTATATCTTTATCTTTGTTGTTGTTG	300				
QY	738 TCCCTTCTGGGCAGAGACTGAGTCTGGAACTCTTTAGACAGATATTGCAAGGAAAGTTAGA	797				
DB	301 TCCCTTCTGGGCAGACAGACAAATGGTATCTTCAACAGATATTAAAGGAAGATAGA	360				
QY	798 TTTCAAATCTGACCGGTGGCTTACTATCTCGAAGCTGCTAAAGATTTTGATCTATAAAT	857				

[illegible]

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VERSION B28263.1 GI:2514229
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 493)
AUTHORS Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
Venter,J.C.
TITLE Use of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopsis Genomic Sequencing
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: T8A20TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 493.
location/Qualifiers
1..493
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T8A20"
/clone_lib="TAMU"
/sex="hermaphrodite"
/notes="Vector: BeLoBACII; Site_1: HindIII; Site_2: HindIII
; Produced by Rod Wing"
BASE COUNT 126 a 110 c 95 g 162 t

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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: ML3F-R.

FEATURES
Source
1. 742
/organism="Solanum tuberosum"
/cultivar="kennebec"
/db_xref="taxon:4113"
/clone="cSTS15M13"
/clone_lib="cSTS"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Various eyes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

BASE COUNT 214 a 128 c 181 g 219 t

ORIGIN
Query Match 23.9%; Score 418; DB 12; Length 742;
Best Local Similarity 74.1%; Pred. No. 1.4e-66;
Matches 529; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 106 GTTCTACCATATCAACACACACAGATTAAGAGATCATTTACCTTCTGGGAAAAAGCTAGGC 165
Db 22 GTTCTCCCTTACAGAACTGAAGAGCTTCAGCAGCTTTACAGATATAGGAAAAAATTAGGG 81
QY 166 CAAGGCCAAATTTGGAAACACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTAGGCC 225
Db 82 CAGGGCCAAATTTGGAAACACCTATTTATGTACAGAAAAATCAACTGCTACTCTTTATGCT 141
QY 226 TGCAAATCGATCCGAGGAAAGCTCGTGTGCGGAGGATTAAGAGATGATGTATGCGGT 285
Db 142 TGCAGAGACTATACAAAGAGAAAGTTGATTGTGAAGAGGATTTATGAGGATTTTGGAGG 201
QY 286 GAGATTCAGATCATGATCATCTCTGAGCATCCAAATGTTGTAGGATCAAGAGGACT 345
Db 202 GAGATTCAGATATGACCAATTTATCTGACACCCAAATGTGTCAGATTAAGGGTACT 261
QY 346 TATGAAGATTCGGTGTGTTGTTGTCATATTTGATGAGGTTTGTGAAGTGGTGTAGCTTTT 405
Db 262 TATGAAGATACCTTATATGTCACATAGTTATGAGCTTTGTCGTGGAGAGCTTTT 321
QY 406 GATCGGATTTCTAAGGTCATTTTATGAGCGTGAAGCTGTCAAGCTTATTAAGACG 465
Db 322 GATAGGATCTGTTGAAAGGGACATTAAGTGAAGGGAGAGCTGCGAAGCTTATTAAGACT 381
QY 466 ATTCTGTGTTGTTGAGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 525
Db 382 ATTCTGTGAGTGTGAGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 441
QY 526 GAGAAATTTCTTTGATATGTCCTTAAGATGATGCTTAAGCTTAAGCTTACGATTTGGT 585
Db 442 GAGAAATTTCTTTGATATGTCCTTAAGATGATGCTTAAGCTTACGATTTGGT 501
QY 586 TTGCT 645
Db 502 CTCTCCGTTTCTACCGCCAGGGAATGTTTCCGATGTTGTTGAGTCTTACTAT 561
QY 646 GTTGACCCAGAGTGTCTAAAGAAATGTTATGACCTGAAATAGATGTTGAGTGTCTGTT 705
Db 562 GTTGACCTGAGTTTACGCAAGCATTTATGACCTGATCTGATGATGATGAGCGCAGGA 621
QY 706 GTTATPCTCTACATTTTACTCAGCGGTGTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCT 765
Db 622 GTTATTTGTACATATTAATCTAGTGGGCTTCCACCTTTTGGGAGAACTAGATGGGA 681
QY 766 ATCTTTACAGATATATCCCAAGGAAGTTAGATTTCAATCTGACCCGTGGCCT 819

Db 682 ATATTCCGCCAGATATTGCAAGCAAAATAGATTGAAATCTGACCATGGCT 735

RESULT 13
BM779035

LOCUS
DEFINITION
BM779035 813 bp mRNA linear EST 04-MAR-2002
EST589610 KV2 Medicago truncatula cDNA clone pkV2-22111, mRNA
sequence.
ACCESSION
BM779035
VERSION
BM779035.1 GI:19108729
KEYWORDS
EST.
SOURCE
barrel medic.
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 813)
AUTHORS
VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Van Aken
S., Utterback,T., Cheung,F., Tsai,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula 48 hr after inoculation with
Sinorhizobium meliloti
Unpublished (2002)
JOURNAL
Contact: VandenBosch K
COMMENT
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@csb.umn.edu
TIGR sequence name: MTABK54TK More information is available at:
www.medicago.org
Seq primer: SKmod (CTA gaa cta gtc gat cc).
FEATURES
Location/Qualifiers
1. 813
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pkV2-22111"
/clone_lib="KV2"
/tissue_type="Seedling roots"
/dev_stage="2 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-da-zap phage using
Ex-assist helper phage and propagated in SOLR cells."

BASE COUNT 229 a 151 c 188 g 245 t

ORIGIN
Query Match 23.0%; Score 402.4; DB 14; Length 813;
Best Local Similarity 74.0%; Pred. No. 9.7e-64;
Matches 536; Conservative 0; Mismatches 186; Indels 2; Gaps 2;

QY 106 GTTCTACCATATCAACACACACAGATTAAGAGATCATTTACCTTCTGGGAAAAAGCTAGGC 165
Db 91 GTTCTCCCTTATGATGATGAAATCTTCGTGAAGTTTACACCTTAGCAGAAACTGGGT 150
QY 166 CAAGGCCAAATTTGGAAACACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTAGGCC 225
Db 151 CAAGGTCAATTTGGGATCATCATCTACTGTCATACACAACTCAACGGGTAGAACCTAGCT 210
QY 226 TGCAAATCGATCCGAGGAAAGCTCGTGTGCGGAGGATTAAGAGATGATGTATGCGGT 285
Db 211 TGCAAATCAATCTCAAGAGAGAGAGCTTTTATGCAAGAGAGGATTTATGATGATGTTGAGA 270
QY 286 GAGATTCAGATCATGATCATCTCTCTGAGCATCCAATGTTGTAGGATCAAGAGGACT 345
Db 271 GAGATTCAGATTAATGACCAATTTGTCGAAATCCAATGTTGTGAGATCCATGGACT 330

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initiation/growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers develop from axillary buds attached to stem explants which placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as p3 in Tanksley lab notebooks."

BASE COUNT	
ORIGIN	
198 a	122 c 204 t
198 a	122 c 162 g

Query Match 23.0%; Score 401.8; DB 13; Length 686;
Best Local Similarity 74.2%; Pred. No. 1.3e-63;
Matches 508; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

	QY	442	GAAGCTGCAAGCTTATTAAAGACGATCTTGTTGGTGTGTGTAGGCCTTGTCATTCTCTGGT	501
	Db			60
		1	GAAGCTGCTAATTTGATCAAACAATTTTGGGGTGGTGGAGCTTGCCATTCATTAGG	
	QY	502	GTTATGCATAGAGATCTCAAAACCTCGAGAAATTTCTTTGTTGTAGTCCCTAAAGATGATGCT	561
	Db			120
		61	GTTATGCACAGATCTAAAGCCTCAGAAATTTCTTTGTTTAGTCTCAAGAGGATGCT	
	QY	562	AAGCTTAAGGCTACCGAATTTGGTTTGCTGCTCTATAAGCCAGGACAATATTATAT	621
	Db			180
		121	GCTCTCAAGGCCACTGATTTTGGCCCTTTCTGTTTTCTATAAGCCAGGTGAACAATTTCT	
	QY	622	GAGCTAGTTGGAAGTCGCTACTATGTGCACCAGAGGTGCTAAAGAAATGTTATGACCT	681
	Db			240
		181	GATGTTGTTGNAAGTCCTTATTATGTGCCCCAGAGGTTTATGCAAGCATTTATGACCT	
	QY	682	GAATATAGATGTGGAGTGCTGGTGTATTCCTCTACATTTTACTCAGCCGGTGTCTCTCCC	741
	Db			300
		241	GAATCAGATGTATGAGTGCAGAGGATTCCTGTACATATTACTTTASTGGTGTCCACCT	
	QY	742	TTCCTGGCAGACACTGAGTCTGGAACTCTTTAGACAGATATGCAAGGGAAGTTAGATTTC	801
	Db			360
		301	TTTTTGGCAGAACAATGATNGGAATTTTCGTGAGATCTGCGAGGCAACTAGATTTA	
	QY	802	AAATCTGACCGCTGGCCTACTATCTCAGAAGTGTCTAAAAGATTGTATCTATAAAATGCTC	861
	Db			420
		361	GAATCGAACCTTGGCCTGGAATTTCAGATAGTGCAAGGATTTGATACGCAAAATCTT	
	QY	862	GAAGAGAGCCCCAAGAAAGCGATTTCTGCTATGAGCCCTGTGTCAACCATGGATTGTC	921
	Db			480
		421	GATAGGAATCCAAGAGGAGGTTAACTGGCCATGAAGTTTGTGCCATCCGTGGATCGTG	
	QY	922	GATGAACAGCACCCACACAGCCCTCTGTATCCAGCAGTCTATCTCGCTCTAAAGCAG	981
	Db			540
		481	GATGACTCAATGACCCCTGATAAACCTCTTGATCTGCGATCTCTTTCACGCCCTCAAGCA	
	QY	982	TTTTCTCAATGAATGAAGATTAAAGAAATGGCATTACGGTAAATTGCTGAGACAGCTTCA	1041
	Db			600
		541	TTCTCAGCAATGAACAAACTAAAGAAATGGCTTTGGTGTGATTCGGAGAGGCTATCA	
	QY	1042	GAGGAAGAAATTTGGAGGCTCTGAAGGAATTTTCAAGATGATAGACAGACACACAGCGGA	1101
	Db			660
		601	GAGAGGAGATTGTTGSCCTCAAGGAGCTATTCAAAATGTTAGACACAGACAATAGTSGA	
	QY	1102	ACGATTACTTTTGAAGAGCTCAAG	1126
	Db			685
		661	AACATAAGCTTTTGAAGAACTAAAAG	

RESULT 15

QY	346	TATGAAGATTCCGGTGTTCCTTCATATGTTATGGAGGTTTGTGAAGGTCGGTGAAGCTTTT	403
Db	331	TACGAGGATTCCGTTTCTCTTCATTTGGTATTATGGAGCTTTGTGAAGGTGGGGAATGTGTT	390
QY	406	GATCGGATGTGTTTCTAAAGGTCATTTTAGTGAGCGCTGAAGCTGTCAAGCTTATTAAAGACG	465
Db	391	GATAGGATGTGCAGAAAGGCAATTATAGTGAGACAAAGCTGCTAAGTGTATTAGAAGT	450
QY	466	ATTCTTGGTGTGTTTGAGGCTTGTCAATCTCTTTGGTGTATGCAATAGAGATCTCAAAGCT	525
Db	451	ATTGTTGAGGTTGTTCAAGCTTGTCAATCTCTTTGGAGTTATGCACAGACACCTTAAAGCT	510
QY	526	GAGAAATTCITGTTTGATAGTCTCAAGATGATGCTAAGCTTAAAGGCTACCGATTTTCGT	585
Db	511	GAGAAATTTTGTGTTGATCTCTGTATGAAGATGCTCTCTCAAAACTATTGATTTTGGT	570
QY	586	TTGTCTGCTCTTATAAAGCCAGACAAATATTTATATGACGTAGTTGGAAGTCCGCTACTAT	645
Db	571	TTGTCTGTTTTTACAGCCAGGTGAATCTTTAGTGATGTTGTTGGAAGCCCATCTAT	630
QY	646	GTTGCACAGAGGTGCTTAAAGAAATGTTATGGACCTGGAATAGATGTGTGGAGTG-CTGG	704
Db	631	GTTGGCCGACAGGCTTGTGCACAAACATATATGGACCTGGAACGACAGCTGTGTGGAGTGCCTGG	690
QY	705	TGTTATCCTCTACATTTTACTACAGCGTGTTCTCCCTTCTGGGCAGACATGAGTCTGG	764
Db	691	TGTTATTTGTGATCATCTATTAGCGGGGTGCCTCCGTTTGGCCCGACGACATCAAG	750
QY	765	AATCTTTAGACAGATATTTCAAGGGGAAGTTAGATTTTCAAACTCTGACCCGTGGCCTACTAT	824
Db	751	GATCTTCAGACAGAT-TTTCAGGAAACACTTGATTTCCGCTCTGAGCCGTGGCCTGGGAT	809
QY	825	CTCA 828	
Db	810	TTCA 813	
RESULT 14			
LOCUS	B1178776	EST519721 cSTE Solanum tuberosum cDNA clone cSTE15P12 5' sequence.	EST 09-JUL
DEFINITION	B1178776	mRNA	linear
ACCESSION	B1178776		
VERSION	B1178776.1	GI:14644587	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum		
ORGANISM	potato.		
REFERENCE			
AUTHORS	Eukaryota; Viridiplantae; streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
	1 (bases 1 to 886)		
	van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R., Cho,J., Chilingo,A., Bougri,O., Buehl,C.R., Ronning,C., Tanksley,S. a Baker,B.		
TITLE	Generation of ESTs from in vitro grown microtubers		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: M13F-R.		
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	/clone_lib="cSTE"		
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	/dev_stage="7, 8 and 10 days"		
	/lab_host="SOLR"		

BQ865474
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DEFINITION QGC5A16.yg.ab1 QG-ABCD1 lettuce salinas Lactuca sativa cDNA clone
QGC5A16, mRNA sequence.
ACCESSION BQ865474
VERSION BQ865474.1 GI:22250939
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 751)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J., Ellison,
P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA.Contig3691, see http://cgpdb.ucdavis.edu/
for details.
Plate: QGC5 row: A column: 16.
FEATURES
Location/Qualifiers
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/clone.lib="QG-ABCD1 lettuce salinas"
/lab_host="E. coli"
/note="Vector: pBRCNDSFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG.LIB=QG-ABCD1 lettuce salinas
TAG.TISSUE=chemical induction
TAG_SEQ=TGATGCGGG"
BASE COUNT 218 a 117 c 180 g 236 t
ORIGIN
Query Match 22.3%; Score 388.8; DB 14; Length 751;
Best Local Similarity 70.9%; Pred. No. 3e-61;
Matches 530; Conservative 0; Mismatches 217; Indels 1; Gaps 1;
QY 287 AGATTCAGATCAATGATCTCTCTGAGCATCCCAATGTTGTAGGATCAAGGACCT 346
DB 1 AGATTCAGATCAATGATCTCTCTGAGCATCCCAATGTTGTAGGATCAAGGACCT 60
QY 347 ATGAAGATCGGTGTGAGGTGTTGTTATGTTAGGAGGTGTTGAGGCTTTTG 406
DB 61 ATGAAGATCGGTGTGAGGTGTTGTTATGTTAGGAGGTGTTGAGGCTTTTG 120
QY 407 ATCGGATGTTCTTAAGGTCATTTAGTGAGCGGTGAAGCTGTCAAGCTTATTAAAGCGA 466
DB 121 ATAGGATTTCAAGAGGACATTACACTGAAAAAAGCAGCTGAGCTTACAAAGCGA 180
QY 467 TTCTTGGTGTGTTGAGGCTGTGTCATCTCTTGGTGTATGATAGATCTCAAGGCTG:526
DB 181 TTGTTGGGTTGTGGAGACTGTGTCATCTTTAGGGGTTATGATCGCGGATTAAAGCCTG 240

QY 527 AGATTTCTTGTGTTAGTCCTAAAGATGATGCTAAGCTTAAGGCTAACGGAATTTGGTT 586
DB 241 AAAATTTCTTGTCTTGTGTAFAAGAAAGAGATTGCGTCTTCAAAACCTATTGATTTGGAT 300
QY 587 TGTCTGTCTTCTATAGCCAGGACAATATTATATGACGTAGTTGGAGTCCGCTACTATG 646
DB 301 TATCGGTTTCTTCAAAACCAGGTGAATCAATTAATGATGTGGTTGGAAGCCCATATTATG 360
QY 647 TTGCACACAGAGGTGCTTAAAGAAATGTTATGACCTGAATAGATGTGTGGAGTCTCGTG 706
DB 361 TTGCACACAGAGTTTGTGAGAAAACGTTATGCGCTGAAGCAGAGCTTTGGAGTCTCGGG 420
QY 707 TTATCTCTTACATTTTACTCAGCGGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 766
DB 421 TTATGTTTATCTTATTAAGTGTGTACCTCCATTTTGGGCTGAAACGAGCAAGGAA 480
QY 767 TCTTTAGACAGATATTGCAAGGGAAGTTAGATTCAATCTGACCCGCTGGCTACTATCT 826
DB 481 TATTTGAACAAGTCTCTCAAGGCGATCTTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 827 CAGAGCTGTCTAAAGATTGATCTATAAATGCTCGAAAGGAGGCCCAAGAAAGCGCATTT 886
DB 541 CTGAGATGCAAAAGATCTTGTAAAGGCAATGCTTATTCGAGACCTTAAAGAGCGATTAA 600
QY 887 CTGCTCATGAAGCCCTTGTGTCAACCATGGATTGCGATGAACAAGCAGCACCACACAAAG 946
DB 601 CTGCACATGAAGTTTATGTCTCATCTTGGGTTCAAGTTGATGGGCTGGCTCCAGACAAG 660
QY 947 CTCTGTATCCAGCACTCTTATCTCGTCTAAAGCAGTTTCTCAATGAATGAATTAAGA 1006
DB 661 CTCTGCACTCTGCAAGTCTTAAGTAGAATGAA-CAATTTTCAGCCCATGAATGAAGCTTTAGA 719
QY 1007 AAATGGCATTACGGGTAATTTGCTGAGAG 1034
DB 720 AAATGGCTTTGAGGGTTTATAGCTGAGAG 747

Search completed: March 26, 2003, 13:10:39
Job time : 3031 secs